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IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

IN RE APPLICATION OF: Adriana S. HEMERLY, et al.

GAU:

SERIAL NO: New Application

EXAMINER:

FILED: Herewith

FOR: PLANT PROTEINS

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REQUEST FOR PRIORITY

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SIR:

☒ Full benefit of the filing date of International PCT application No. PCT/EP00/06401, filed July 5, 2000, is claimed pursuant to the provisions of **35 U.S.C. §120**.

☐ Full benefit of the filing date of U.S. Provisional Application Serial Number , filed , is claimed pursuant to the provisions of **35 U.S.C. §119(e)**.

☒ Applicants claim any right to priority from any earlier filed applications to which they may be entitled pursuant to the provisions of **35 U.S.C. §119**, as noted below.

In the matter of the above-identified application for patent, notice is hereby given that the applicants claim as priority:

COUNTRY	APPLICATION NUMBER	MONTH/DAY/YEAR
EUROPE	99202214.5	JULY 5, 1999

Certified copies of the corresponding Convention Application(s)

☒ are submitted herewith

☐ will be submitted prior to payment of the Final Fee

☐ were filed in prior application Serial No. filed

☐ were submitted to the International Bureau in PCT Application Number
Receipt of the certified copies by the International Bureau in a timely manner under PCT Rule 17.1(a) has been acknowledged as evidenced by the attached PCT/IB/304.

☐ (A) Application Serial No.(s) were filed in prior application Serial No. filed ; and

☐ (B) Application Serial No.(s)

- ☐ are submitted herewith
- ☐ will be submitted prior to payment of the Final Fee

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Bescheinigung | Certificate | Attestation

Die angehefteten Unterlagen stimmen mit der ursprünglich eingereichten Fassung der auf dem nächsten Blatt bezeichneten europäischen Patentanmeldung überein.

The attached documents are exact copies of the European patent application described on the following page, as originally filed.

Les documents fixés à cette attestation sont conformes à la version initialement déposée de la demande de brevet européen spécifiée à la page suivante.

Patentanmeldung Nr. | Patent application No. | Demande de brevet n°

99202214.5

Der Präsident des Europäischen Patentamts;
Im Auftrag

For the President of the European Patent Office

Le Président de l'Office européen des brevets
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Title: Plant proteins.

The present invention relates to at least partially purified protein, capable of modulating the DNA replication in plants, muteins thereof, DNA coding therefor and to a method to confer to one or more plant cells the capacity to provide such a protein or mutein. The invention also relates to plants, comprising the said DNA and the progeny thereof.

The regulation of the cell cycle in plants is poorly understood. Most of the knowledge regarding the regulation of DNA replication, also known as the S-phase of the cell cycle regulation originates from experimental data obtained in yeast and mammalian cells. However, the importance to understand the cell cycle regulation in plant cells has become increasingly important in agriculture, e.g. to control growth of plants at stress conditions, to obtain resistance against parasites that block or modulate the cell cycle regulation, or to improve the yield of agriculturally important crops. Further, one might be interested to intervene in the cell cycle regulation by allowing further rounds of DNA replication, but simultaneously preventing further cell cycle progress by blocking the subsequent mitosis. In this way, cells may be obtained having multiple sets of their genetic material, so that plants with a high rate of endoreduplication may be generated. The term "endoreduplication" means recurrent DNA replication without consequent mitosis and cytokinesis.

From experiments in yeast, it is known that DNA replication and mitosis are coupled events in the cell cycle. Paulovich et al., 1997; Cell 88, 315-321. Genetic studies in yeast for example suggest that the CDC7 serine-threonine kinase plays a role in the initiation of DNA synthesis. Evidence has been presented that CDC7 is apparently directly involved in the activation of individual early- as well as late replication origins during S-phase (Bousset and Diffley, 1998, Genes Dev 12, 480-490; Donaldson et al., 1998, Genes Dev 12, 491-501). The protein levels of CDC7 are constant during the cell cycle. Activation of CDC7 as a kinase occurs at the G1/S transition of the cell cycle and is dependent on the binding with another factor, DBF4, at the G1/S transition of the cell cycle,

probably by phosphorylating proteins at the origins (Kitada et al, 1992; Genetics 131: 21-29, Lei et al; Genes and Development 11, 3365-3374, 1997). In order to function as a kinase, the CDC7 kinase may be a substrate for one or more phosphorylation events. Overexpressed kinase-negative mutants of CDC7 arrest yeast cells in the G1 to S transition and inhibit growth. Further experiments showed that the inactivation of wild-type CDC7 function probably can be explained through titration of DBF4 by the inactive cdc7 mutant proteins (Ohtoshi et al., 1997, Mol Gen Genet 254, 562-570). In addition to mechanisms to control the onset of DNA replication, other mechanisms contribute to restrict DNA replication to occur only once during the cell cycle. For example, the CDC16, CDC23 and CDC27 proteins are part of a high molecular weight complex, known as the anaphase promoting complex (APC) or cyclosome, (see Romanowski and Madine, Trends in Cell Biology 6, 184-188, 1996, and Wuarin and Nurse, Cell 85, 785-787 (1996), both incorporated herein by reference). The complex in yeast is composed of at least 8 proteins, the TPR (tetratricopeptide repeat) containing proteins CDC16, CDC23 and CDC27, and five other subunits named APC1, APC2, APC4, APC5 and APC7 (Peters et al. 1996, Science 274, 1199-1201). The APC targets its substrates for proteolytic degradation by catalyzing the ligation of ubiquitin molecules to these substrates. APC-dependent proteolysis is required for the separation of the sister chromatids at meta- to anaphase transition and for the final exit from mitosis. Among the APC-substrates are the anaphase inhibitor protein Pds1p and mitotic cyclins such as cyclin B, respectively (Ciosk et al. 1998, Cell 93, 1067-1076; Cohen-Fix et al. 1996, Genes Dev 10, 3081-3093; Sudakin et al. 1995, Mol Biol Cell 6, 185-198; Jorgensen et al. 1998, Mol Cell Biol 18, 468-476; Townsley and Ruderman 1998, Trends Cell Biol 8, 238-244). To become active as a ubiquitin-ligase, at least CDC16, CDC23 and CDC27 need to be phosphorylated in the M-phase (Ollendorf and Donoghue 1997, J Biol Chem 272, 32011-32018). Activated APC persists throughout G1 of the subsequent cell cycle to prevent premature appearance of B-type cyclins which would result in an uncontrolled entry into S-phase (Irniger and Nasmyth 1997, J Cell Sci 110, 1523-1531). It has been demonstrated in yeast that mutations in

either of at least two of the APC components, CDC16 and CDC27, can result in DNA overreplication without intervening passages through M-phases (Heichman and Roberts 1996, Cell 85, 39-48). CDC16,CDC23 and CDC27 all are tetratricopeptide repeat (TPR) containing proteins. A suggested minimal consensus sequence of the TPR motif is as follows: X_3-W-X_2-L-G-X_2-Y-X_8-A-X_3-F-X_2-A-X_4-P-X_2 (Lamb et al. 1994, EMBO J 13, 4321-4328; X denotes any amino acid, X_n a stretch of n of such amino acids). However, the consensus residues can exhibit significant degeneracy and little or no homology is present in non-consensus residues. The hydrophobicity and size of the consensus residues, rather than their identity, seems to be important. TPR motifs are present in a wide variety of proteins functional in yeast and higher eukaryotes in mitosis (including the APC protein components CDC16, CDC23 and CDC27), transcription, splicing, protein import and neurogenesis (Goebl and Yanagida 1991, Trends Biochem Sci 16, 173-177). The TPR forms a α-helical structure, tandem repeats organize into a superhelical structure ideally suited as interfaces for protein recognition (Groves and Barford 1999, Curr Opin Struct Biol 9, 383-389). Within the α-helix, two amphipathic domains are usually present, one at the NH_2-terminus and the other near the COOH-terminus (Sikorski et al. 1990, Cell 60 ,307-317).

In order to understand the mechanisms playing a role in plant cell cycle regulation, in particular the DNA replication, and to understand endoreduplication in plants, the present inventors isolated several novel plant DNA sequences, coding for novel proteins, or novel amino acid sequences thereof involved in the modulation of DNA replication, using degenerated PCR primers based on known genomic or cDNA sequences, e.g. of yeast, mammals and insects.

"Capable of modulating the DNA replication in plants" is to be understood as the capacity of a protein to alter the natural DNA replication mechanism in the said plant, e.g. by up- or down-regulation of the DNA replication in a way, different from the natural situation, or to a higher or lower extent with respect to the natural situation. The natural situation is to be understood as the situation wherein DNA replication takes place in plants, in which the DNA replication machinery is not affected by the introduction of foreign

genetic material. Such altering includes mediating e.g. the onset of DNA replication, the rate and extent of DNA replication, the timing of DNA replication in the cell cycle, coupling or uncoupling DNA replication with/from actual subsequent cell division etcetera.

Proteins

By using degenerated oligonucleotides as amplification primers, based on conserved sequence regions of the CDC7 homologue gene of *Saccharomyces cerevisiae* and *Schizosaccharomyces pombe* and on conserved sequence regions of the CDC27 homologue genes of *Schizosaccharomyces pombe* and from *Aspergillus Nidulans*, drosophila and human, the present inventors surprisingly found such novel proteins and amino acid sequences. Reference is made to the examples.

Thus, novel cDNAs and proteins comprising one or more novel amino acid sequences were found. The present invention therefore relates in the first place to an at least partially purified protein, capable of modulating DNA replication in plants, at least comprising in the amino acid sequence

a) one or more of the amino acid sequences chosen from the group consisting of those, given by SEQ ID NOS 2, 3 and 4,

b) one or more of the amino acid sequences chosen from the group consisting of those, given by SEQ ID NOS 6 and 7,

c) one or more amino acid sequences having at least 50% amino acid identity with those of a), or

d) one or more amino acid sequences having at least 50% amino acid identity with those of b).

By using degenerated CDC7 oligonucleotides to amplify a PCR fragment as is indicated above and will be further detailed in the examples, a novel *Arabidopsis* cDNA comprising coding sequence of an novel *Arabidopsis* CDC7 homologue gene was found (SEQ ID NO 8). By comparison of the said sequences with sequences of the EMBL and EMBLnew databanks, a genomic *Arabidopsis thaliana* sequence was found (accession number Z97342). In this known genomic sequence however, only 11 exons were identified. The novel DNA according to the present invention however clearly indicated the presence of 3

additional coding sequences coding for novel amino acid sequences (SEQ ID NO 2, 3, 4) being part of a DNA replication modulating plant protein, homologous to yeast CDC7.

The novel amino acid sequence SEQ ID No 2 (GYGIVYKATRKTDGTEFAIK) is located in two highly conserved domains in protein kinases, Domain I and II (Hawks et al., 1988, Science 241, 42-52). The sequence GYGIV is part of the nucleotide (ATP) binding domain, also known as Domain I in protein kinases. Domain I is part of the catalytic domain of protein kinases. The Glycines (G) are believed to form an elbow around the nucleotide, and the Valine (V) is believed to contribute to positioning of the Glycines. The first Glycine and the Valine are invariant in all protein kinases. The second Glycine is almost invariant.

The sequence AIK in the same peptide is also highly conserved and it is located in Domain II, which is also part of the catalytic domain. The Alanine (A) and the Lysine (K) are invariant in all kinases, and the Isoleucine is highly conserved. The Lysine residue appears to be involved in mediating the phosphotransfer reaction (Hawks et al, 1988).

This exon is responsible for the kinase activity of CDC 7. This implies that the CDC 7 coding sequence from the state of the art is not functional.

The novel exon encoded by amino acid sequence SEQ ID No 3 (DVIEKKDGPCSGTKGFRAPE) is part of Domain VIII of protein kinases. Mutagenesis has implicated a role of this domain in the catalytic activity (Hawks et al., 1988). In the sequence TKGFRAPE, the amino acids Threonine (T), Phenylalanine and Alanine (A) are highly conserved, and the Glutamic Acid (E) is invariant. Moreover, substitution of the corresponding threonine in the yeast CDC7 homologue (position 281 of the yeast CDC7; position 722 in SEQ ID No 1) to a glutamate resulted in a dominant-negative CDC7mutant (Ohtoshi et al. 1997, Mol Gen Genet 254, 562-570).

The novel exon, encoded by amino acid sequences SEQ ID No 4 (NIKDIAQLRGSEELWEVAKLHNRESSFPK) is located in Domain XI of protein kinases, and that in the peptide, the first Leucine (L), and the second Lysine (K) are highly conserved and therefore are believed to be quite important for the correct activity of the protein.

In addition, using degenerated CDC27 oligonucleotides, an *Arabidopsis thaliana* cDNA sequence was found, which upon comparison in the above mentioned databanks, showed high homology with an *Arabidopsis thaliana* genomic DNA sequence (accession number AC 001645). Again, the coding sequence (SEQ ID NO 9), found by the present inventors, indicated the presence of two additional coding regions in the *Arabidopsis* CDC27, the gene, corresponding with the amino acid sequences given by SEQ ID NOS 6 and 7. Thus, novel DNA replication modulating proteins in plants were found, comprising one or more of the above mentioned novel amino acid sequences.

The novel exon encoded by amino acid sequence SEQ ID No 6 (VNLQLLARCYLSNQAYSAYYILK) is part of a unique NH_2-terminal domain conserved in CDC27 homologues of different origin. The unique domain is located upstream of the NH_2-terminal TPR unit of CDC27 (Tugendreich et al. 1993, Proc Natl Acad Sci USA 90, 10031-10035). The role of this domain is currently not known, but its conservation suggests that it is indispensable for CDC27 function. The NH_2-terminal TPR of CDC27 is not tandemly repeated and spans the amino acid residues 174 to 202 in SEQ ID No 5. Proteins, comprising this novel exon sequence according to the invention may therefore promote APC-substrate action and therewith allowing DNA-replication. On the other hand, a peptide comprising the novel exon sequence may be used to occupy the binding region of the substrates for the APC complex, and therewith inhibiting the complex-substrate interactions, resulting in inactivation of APC and to polyploiddization/endoreduplication.

The novel amino acid sequence SEQ ID No 7 (AYMERLILPDELVTEENL) is located just after the last (10th) TPR of CDC27 spanning the amino acid residues 670-703 in SEQ ID No 5. Carboxy-terminal extensions downstream from this 10^{th} TPR and variable in length and sequence are common in all known CDC27 proteins. However, the sequence SEQ ID No 7 shows 50 and 55% homology to the corresponding regions of the CDC27 homologues of *Schizosaccaromyces pombe* and *Aspergillus nidulans*, respectively. Moreover, and previously not recognized, the 25 carboxy-terminal amino acids (ending with SEQ ID No 7) immediately downstream of the 10^{th} TPR compose a sequence unit sharing characteristics of a TPR-domain: 1)

secondary structure prediction using the Chou-Fasman algorithm (Chou and Fasman 1978, Annu Rev Biochem 47, 251-276) reveals the possibility of the 25 amino acid stretch to form an α-helix, 2) applying the Eisenberg algorithm (Eisenberg 1984, Annu Rev Biochem 53, 595-623) furthermore predicts the existence of two amphipathic domains within the α-helix formed by the same 25 amino acid sequence, 3) a truncated TPR of 27 amino acids exists in the SKI3 antiviral protein of *Saccharomyces cerevisiae* (Rhee et al. 1989, Yeast 5, 149-158). Remarkably, three consecutive core amino acids of this TPR, RLI, are also present in SEQ ID No 7 and, although very limited, some further homology can be discovered. Thus, although circumstancial, these data may suggest that SEQ ID No 7 is part of a truncated TPR. If so, the block of tandemly repeated TPRs in CDC27 should be extended from 9 (spanning amino acids 406 to 703 in SEQ ID No 5) to 10 (amino acids 704 to 728 in SEQ ID No 5). Interestingly, it has been suggested that a dimer of the basic 34 amino acid TPR repeat is the more common evolutionary unit (Sikorski et al. 1990, Cell 60, 307-317).

The effect of mutations in one out of the tandem series of TPRs can be very specific. For instance, a point mutation in the most highly conserved 7th TPR domain of yeast CDC27 results in a greatly reduced affinity for interaction with yeast CDC23, but not for interaction with yeast CDC16 or wild-type CDC27. A single amino acid insertion in the same domain destroys the α-helix and abolishes interaction with wild-type CDC27 as well as CDC16 (Lamb et al. 1994, EMBO J 13, 4321-4328). Moreover, detailed experiments with the human TPR-containing CDC16 and CDC27 homologues and another TPR-containing protein regulating the APC-activity, PP5, revealed that TPR proteins display discriminate binding to other TPR proteins. More specifically for CDC27, deletion of the first TPR domain in this protein abolishes CDC16 binding, but not PP5 binding (Ollendorf and Donoghue 1997, J Biol Chem 272, 32011-32018). Mutagenesis studies with the yeast CDC23 showed that only a few residues in or near the most canonical 6th TPR unit result in temperature-sensitive defects (Sikorski et al. 1993, Mol Cell Biol 13, 1212-1221). Separate TPR domains thus seem to be involved in specific interactions with other proteins and only

very limited alterations in these domains seem to be tolerated. Any erroneous modulation of APC activity, e.g. by mutations in SEQ ID No 6 as part of a conserved sequence in CDC27 proteins and/or SEQ ID No 7 being a putative novel truncated TPR motif in CDC27, will likely result in loss of control over normal DNA replication cycles via the mechanisms described above. Mutations in CDC27 can indeed trigger DNA overreplication and thus the generation of polyploid cells (Heichmann and Roberts 1996, Cell 85, 39-48). Such endoreduplication might be related to cell expansion (Traas et al. 1998, Curr Opin Plant Biol 1, 498-503) and, thus, a higher storage capacity in such polyploid cells. This advantageous property is highly desired in crop plants or parts of plants such as seeds, roots, tubers and fruits.

Modulating the said amino acid sequence would impair the formation of functional APC, whereas cdc27 comprising such a mutation would still be able to interact with the substrate and therewith titrating the substrate out, leading to the abolishment of APC-function in the plant cell, resulting in polyploid cells.

It is to be understood, that DNA replication modulating proteins according to the present invention, comprising one or more of the above mentioned amino acid sequences, or having 80% amino acid identity therewith, may originate from plant species as well as from other species as long as the said proteins are capable of modulating DNA replication in one or more plant species.

The term "protein" is to be understood as any amino acid sequence having a biological function, optionally modified by e.g. glycosylation. The protein according to the present invention preferably comprises one or more of the amino acid sequences according to c) or d), the respective amino acid identity preferably being at least 50% .

The term "protein" includes single-chain polypeptide molecules as well as multiple-polypeptide complexes where individual constituent polypeptides are linked by covalent or non-covalent means. The term "polypeptide" includes peptides of two or more amino acids in length, typically having more than 5, 10 or 20 amino acids.

It will be understood that amino acid sequences of the invention are not limited to the sequences obtained from the particular protein but also include homologous sequences obtained from any source, for example related plant proteins, cellular homologues and synthetic peptides, as well as variants or derivatives thereof.

Thus, the present invention covers variants, homologues or derivatives of the amino acid sequences of the present invention, as well as variants, homologues or derivatives of the nucleotide sequence coding for the amino acid sequences of the present invention.

In the context of the present invention, a homologous sequence is taken to include an amino acid sequence which is at least 50, 60, 70, 80 or 90% identical, preferably at least 95 or 98% identical at the amino acid level over at least 18, preferably all amino acids within the sequences as shown in SEQ ID Nos 2, 3, 4, 6 and 7 in the sequence listing herein. In particular, homology should typically be considered with respect to those regions of the sequence known to be essential for the above discussed functions of the novel amino acid sequences rather than non-essential neighbouring sequences. Although homology can also be considered in terms of similarity (i.e. amino acid residues having similar chemical properties/ functions), in the context of the present invention it is preferred to express homology in terms of sequence identity.

Homology comparisons can be conducted by eye, or more usually, with the aid of readily available sequence comparison programs. These commercially available computer programs can calculate % homology between two or more sequences.

% Homology may be calculated over contiguous sequences, i.e. one sequence is aligned with the other sequence and each amino acid in one sequence directly compared with the corresponding amino acid in the other sequence, one residue at a time. This is called an "ungapped" alignment. Typically, such ungapped alignments are performed only over a relatively short number of residues (for example less than 50 contiguous amino acids).

Although this is a very simple and consistent method, it fails to take into consideration that, for example, in an otherwise identical pair of sequences, one insertion or

deletion will cause the following amino acid residues to be put out of alignment, thus potentially resulting in a large reduction in % homology when a global alignment is performed. Consequently, most sequence comparison methods are designed to produce optimal alignments that take into consideration possible insertions and deletions without penalising unduly the overall homology score. This is achieved by inserting "gaps" in the sequence alignment to try to maximise local homology.

However, these more complex methods assign "gap penalties" to each gap that occurs in the alignment so that, for the same number of identical amino acids, a sequence alignment with as few gaps as possible - reflecting higher relatedness between the two compared sequences - will achieve a higher score than one with many gaps. "Affine gap costs" are typically used that charge a relatively high cost for the existence of a gap and a smaller penalty for each subsequent residue in the gap. This is the most commonly used gap scoring system. High gap penalties will of course produce optimised alignments with fewer gaps. Most alignment programs allow the gap penalties to be modified. However, it is preferred to use the default values when using such software for sequence comparisons. For example when using the GCG Wisconsin Bestfit package (see below) the default gap penalty for amino acid sequences is -12 for a gap and -4 for each extension.

Calculation of maximum % homology therefore firstly requires the production of an optimal alignment, taking into consideration gap penalties. A suitable computer program for carrying out such an alignment is the GCG Wisconsin Bestfit package (University of Wisconsin, U.S.A.; Devereux *et al.*, 1984, Nucleic Acids Research 12:387). Examples of other software than can perform sequence comparisons include, but are not limited to, the BLAST package (see http://www.ncbi.nih.gov/BLAST/), FASTA (Atschul *et al.*, 1990, J. Mol. Biol., 403-410; FASTA is available for online searching at, for example, http://www.2.ebi.ac.uk.fasta3) and the GENEWORKS suite of comparison tools. However it is preferred to use the GCG Bestfit program.

Although the final % homology can be measured in terms of identity, the alignment process itself is typically not based on an all-or-nothing pair comparison. Instead, a scaled

similarity score matrix is generally used that assigns scores to each pairwise comparison based on chemical similarity or evolutionary distance. An example of such a matrix commonly used is the BLOSUM62 matrix - the default matrix for the BLAST suite of programs. GCG Wisconsin programs generally use either the public default values or a custom symbol comparison table if supplied (see user manual for further details). It is preferred to use the public default values for the GCG package, or in the case of other software, the default matrix, such as BLOSUM62.

Once the software has produced an optimal alignment, it is possible to calculate % homology, preferably % sequence identity. The software typically does this as part of the sequence comparison and generates a numerical result.

Polypeptide Variants and Derivatives

The terms "variant" or "derivative" in relation to the amino acid sequences of the present invention includes any substitution of, variation of, modification of, replacement of, deletion of or addition of one (or more) amino acids from or to the sequence providing the resultant amino acid sequence has similar activity as the polypeptides presented in the sequence listings.

The sequences of the invention may be modified for use in the present invention. Typically, modifications are made that maintain the activity of the sequence. Amino acid substitutions may be made, for example from 1, 2 or 3 to 10, 20 or 30 substitutions provided that the modified sequence retains the relevant activity. E.g. the kinase activity should be maintained in such a variant of a peptide according to the invention comprising SEQ ID NO 2. Amino acid substitutions may include the use of non-naturally occurring analogues, for example to increase blood plasma half-life of a therapeutically administered polypeptide.

Conservative substitutions may be made, for example according to the Table below. Amino acids in the same block in the second column and preferably in the same line in the third column may be substituted for each other:

ALIPHATIC	Non-polar	G A P
		I L V
	Polar - uncharged	C S T M
		N Q
	Polar - charged	D E
		K R
AROMATIC		H F W Y

Proteins of the invention are typically made by recombinant means. However they may also be made by synthetic means using techniques well known to skilled persons such as solid phase synthesis. Proteins of the invention may also be produced as fusion proteins, for example to aid in extraction and purification. Examples of fusion protein partners include glutathione-S-transferase (GST), 6xHis, GAL4 (DNA binding and/or transcriptional activation domains) and β-galactosidase. It may also be convenient to include a proteolytic cleavage site between the fusion protein partner and the protein sequence of interest to allow removal of fusion protein sequences. Preferably the fusion protein will not hinder the function of the protein of interest sequence.

Proteins of the invention may be in a substantially isolated form. It will be understood that the protein may be mixed with carriers or diluents which will not interfere with the intended purpose of the protein and still be regarded as substantially isolated. A protein of the invention may also be in a substantially purified form, in which case it will generally comprise the protein in a preparation in which more than 90%, e.g. 95%, 98% or 99% of the protein in the preparation is a protein of the invention.

In a special embodiment, the protein according to the present invention comprises the amino acid sequence as given in SEQ ID NO 1 or NO 5, or has at least 80% preferably at least 90% amino acid identity with one of the said sequences. SEQ ID NO 1 relates to the complete amino acid sequence (889 AA) of the novel CDC7 protein according to the present invention comprising SEQ ID NOS 2, 3 and 4 (AA 411-430, 710-729, 767-795). SEQ ID NO 5 is the complete amino acid sequence (728 AA)

of the novel plant CDC27 comprising SEQ ID NOS 6 and 7 (AA 37-60 and AA 710-727 respectively).

Although the proteins according to the present invention may be of non-plant origin, as is indicated above, the protein according to the present invention is preferably a plant protein, more preferably a CDC7 or CDC27 protein, or a functional analogue thereof. A functional analogue is to be understood as any protein or peptide having similar biological effects as a plant CDC7 protein or a CDC27 protein, irrespectively of the origin thereof.

Mutein

In another embodiment, the present invention relates to a mutein of the protein according to the present invention, said mutein comprising at least one amino acid substitution, deletion or addition, affecting the DNA replicative effect of the said protein.

As is already indicated above, the proteins according to the present invention are of high interest for an improvement of e.g. agricultural crops or parasite resistance. By substituting, deleting or adding amino acids to the protein according to the present invention, the modulating effect thereof can be affected, which may lead to desirable or improved properties of the protein.

In particular, DNA replication modulating proteins according to the invention may be activated or deactivated by a phosphorylation-dephosphorylation mechanism, being a known regulatory mechanisms for many cell cycle proteins. Therefore, in a further embodiment of the present invention, one of the phosphorylatable amino acids of the protein according to the present invention is deleted or substituted by one or more non-phospohorylatable amino acids, which may lead to loss of susceptibility of phosphorylation and function.

In particular, the said substitutions deletions or additions may be situated within or flanking the amino acid sequence, as given by SEQ ID NOS 2, 3, 4, 6 or 7 (or having at least 50% amino acid identity therewith).

DNA replicating modulating proteins according to the invention may also comprise one or more tetratricopeptide repeat (TPR) domains. Such domains have been identified in

CDC27 (amino acid regions 174-202, 403-431, 432-465, 466-499, 500-533, 534-567, 568-601, 602-635, 636-669, 670-703 in SEQ ID No 5; delineation of regions based on the yeast CDC27 homologue; Lamb et al. 1994, EMBO J 13, 4321-4328) as well as in CDC16, CDC23 and many other proteins (Goebl and Yanagida 1991, Trends Biochem Sci 16, 173-177). The function of these TPR domains is to enable the protein to interact with other proteins in the anaphase promoting complex (APC). In the CDC27 protein according to the present invention, a novel TPR or TPR-like domain has been identified which includes SEQ ID No 7. Mutation analysis in TPR domains of yeast CDC27 has revealed that intact TPRs are necessary for CDC27 function (Lamb et al. 1984, EMBO J 13, 4321-4328) and, thus, also for a functional APC. In the absence of CDC27 function, DNA synthesis becomes uncoupled from cell cycle progression resulting in the establishment of polyploid cells (Heichman and Roberts 1996, Cell 85, 39-48).

Peptides

Further, the present invention relates to a peptide, comprising

a) one or more of the amino acid sequences chosen from the group consisting of those given by SEQ ID NOS 2, 3 and 4,

b) one or more of the amino acid sequences chosen from the group consisting of those, given by SEQ ID NOS 6 and 7,

c) one or more amino acid sequences having at least 80 % amino acid identity with those of a), or

d) one or more amino acid sequences having at least 80% amino acid identity with those of b).

These peptides, firstly identified by the present inventors, are or maybe part of important regulatory sites for binding cellular factors or being a substrate for activating/ deactivating mechanisms, such as phosphorylation.

Antibodies

Furthermore, the present invention relates to antibodies specifically recognizing a cell cycle interacting protein according to the invention or parts, i.e. specific fragments

or epitopes, of such a protein. The antibodies of the invention can be used to identify and isolate other cell cycle interacting proteins and genes in any organism, preferably plants. These antibodies can be monoclonal antibodies, polyclonal antibodies or synthetic antibodies as well as fragments of antibodies, such as Fab, Fv or scFv fragments etc. Monoclonal antibodies can be prepared, for example, by the techniques as originally described in Köhler and Milstein, Nature 256 (1975), 495, and Galfré, J. Meth. Enzymol. 73 (1981), 3, which comprise the fusion of mouse myeloma cells to spleen cells derived from immunized mammals. Furthermore, antibodies or fragments thereof to the aforementioned peptides can be obtained by using methods which are described, e.g., in Harlow and Lane "Antibodies, A Laboratory Manual", CSH Press, Cold Spring Harbor, 1988. These antibodies can be used, for example, for the immunoprecipitation and immunolocalization of proteins according to the invention as well as for the monitoring of the synthesis of such proteins, for example, in recombinant organisms, and for the identification of compounds interacting with the protein according to the invention. For example, surface plasmon resonance as employed in the BIAcore system can be used to increase the efficiency of phage antibodies selections, yielding a high increment of affinity from a single library of phage antibodies which bind to an epitope of the protein of the invention (Schier, Human Antibodies Hybridomas 7 (1996), 97-105; Malmborg, J. Immunol. Methods 183 (1995), 7-13). In many cases, the binding phenomena of antibodies to antigens is equivalent to other ligand/anti-ligand binding.

DNA sequences

Further, the present invention relates to a non-genomic DNA sequence, coding for a protein or mutein or peptide according to the present invention, or a DNA sequence having a sequence homology of at least 75% with the said sequence, or to the complementary sequence thereof. Also DNA sequences having at least 75% homology with the above mentioned DNA sequences are encompassed within the invention. These sequences are particularly useful in the generation of DNA vectors to multiply the DNA sequence or to introduce the said sequence in

a host organism, in order to obtain the encoded protein. Further said sequences or parts thereof are advantageously used to identify and isolate homologous sequences from other biological species.

The DNA sequence is preferably substantially free of sequences intervening the coding sequence, and is preferably cDNA.

DNA-sequences of the invention comprise nucleic acid sequences encoding the amino acid sequences of the invention. It will be understood by a skilled person that numerous different polynucleotides can encode the same polypeptide as a result of the degeneracy of the genetic code. In addition, it is to be understood that skilled persons may, using routine techniques, make nucleotide substitutions that do not affect the polypeptide sequence encoded by the polynucleotides of the invention to reflect the codon usage of any particular host organism in which the polypeptides of the invention are to be expressed.

Polynucleotides of the invention may comprise DNA or RNA. They may be single-stranded or double-stranded. They may also be polynucleotides which include within them synthetic or modified nucleotides. A number of different types of modification to oligonucleotides are known in the art. These include methylphosphonate and phosphorothioate backbones, addition of acridine or polylysine chains at the 3' and/or 5' ends of the molecule. For the purposes of the present invention, it is to be understood that the polynucleotides described herein may be modified by any method available in the art. Such modifications may be carried out in order to enhance the *in vivo* activity or life span of polynucleotides of the invention.

The terms "variant", "homologue" or "derivative" in relation to the nucleotide sequence of the present invention include any substitution of, variation of, modification of, replacement of, deletion of or addition of one (or more) nucleic acid from or to the sequence providing the resultant nucleotide sequence codes for a polypeptide, preferably having at least the same activity as sequences presented in the sequence listings.

As indicated above, with respect to sequence homology, preferably there is at least 75%, more preferably at least 85%, more preferably at least 90% homology to the sequences shown in the sequence listing herein. More preferably there is at least 95%, more preferably at least 98%, homology. Nucleotide homology comparisons may be conducted as described above. A preferred sequence comparison program is the GCG Winsconsin Bestfit program described above. The default scoring matrix has a match value of 10 for each identical nucleotide and -9 for each mismatch. The default gap creation penalty is -50 and the default gap extension penalty is -3 for each nucleotide.

The present invention also encompasses nucleotide sequences that are capable of hybridising selectively to the sequences presented herein, or any variant, fragment or derivative thereof, or to the complement of any of the above. Nucleotide sequences are preferably at least 15 nucleotides in length, more preferably at least 20, 30, 40 or 50 nucleotides in length.

The term "hybridization" as used herein shall include "the process by which a strand of nucleic acid joins with a complementary strand through base pairing" as well as the process of amplification as carried out in polymerase chain reaction technologies.

Polynucleotides of the invention capable of selectively hybridising to the nucleotide sequences presented herein, or to their complement, will be generally at least 70%, preferably at least 80 or 90% and more preferably at least 95% or 98% homologous to the corresponding nucleotide sequences presented herein over a region of at least 20, preferably at least 25 or 30, for instance at least 40, 60 or 100 or more contiguous nucleotides. Preferred polynucleotides of the invention will comprise regions preferably at least 80 or 90% and more preferably at least 95% homologous to nucleotides (1229-1291), (2126-2187) or (2298-2385) of SEQ ID No 8 or (109-181) or (2128-2181) of SEQ ID No 9.

Hybridization conditions are based on the melting temperature (Tm) of the nucleic acid binding complex, as taught in Berger and Kimmel (1987, Guide to Molecular Cloning Techniques, Methods in Enzymology, Vol 152, Academic Press, San

Diego CA), and confer a defined "stringency" as explained below.

Maximum stringency typically occurs at about Tm-5°C (5°C below the Tm of the probe); high stringency at about 5°C to 10°C below Tm; intermediate stringency at about 10°C to 20°C below Tm; and low stringency at about 20°C to 25°C below Tm. As will be understood by those of skill in the art, a maximum stringency hybridization can be used to identify or detect identical polynucleotide sequences while an intermediate (or low) stringency hybridization can be used to identify or detect similar or related polynucleotide sequences.

In a preferred aspect, the present invention covers nucleotide sequences that can hybridise to the nucleotide sequence of the present invention under stringent conditions (e.g. 65°C and 0.1xSSC {1xSSC = 0.15 M NaCl, 0.015 M Na_3 Citrate pH 7.0).

Where the polynucleotide of the invention is double-stranded, both strands of the duplex, either individually or in combination, are encompassed by the present invention. Where the polynucleotide is single-stranded, it is to be understood that the complementary sequence of that polynucleotide is also included within the scope of the present invention.

Polynucleotides which are not 100% homologous to the sequences of the present invention but fall within the scope of the invention can be obtained in a number of ways. Other variants of the sequences described herein may be obtained for example by probing DNA libraries made from a range of individuals, for example individuals from different populations. In addition, other viral/bacterial, or cellular homologues particularly cellular homologues found in plant cells, may be obtained and such homologues and fragments thereof in general will be capable of selectively hybridising to the sequences shown in the sequence listing herein. Such sequences may be obtained by probing cDNA libraries made from or genomic DNA libraries from other animal species, and probing such libraries with probes comprising all or part of SEQ ID Nos 8 or 9 under conditions of medium to high stringency. Similar considerations apply to obtaining species homologues and allelic variants of the polypeptide or nucleotide sequences of the invention.

Variants and strain/species homologues may also be obtained using degenerate PCR which will use primers designed to target sequences within the variants and homologues encoding conserved amino acid sequences within the sequences of the present invention. Conserved sequences can be predicted, for example, by aligning the amino acid sequences from several variants/homologues. Sequence alignments can be performed using computer software known in the art. For example the GCG Wisconsin PileUp program is widely used.

The primers used in degenerate PCR will contain one or more degenerate positions and will be used at stringency conditions lower than those used for cloning sequences with single sequence primers against known sequences.

Alternatively, such polynucleotides may be obtained by site directed mutagenesis of characterised sequences, such as SEQ ID No 8 or 9. This may be useful where for example silent codon changes are required to sequences to optimise codon preferences for a particular host cell in which the polynucleotide sequences are being expressed. Other sequence changes may be desired in order to introduce restriction enzyme recognition sites, or to alter the property or function of the polypeptides encoded by the polynucleotides.

Polynucleotides of the invention may be used to produce a primer, e.g. a PCR primer, a primer for an alternative amplification reaction, a probe e.g. labelled with a revealing label by conventional means using radioactive or non-radioactive labels, or the polynucleotides may be cloned into vectors. Such primers, probes and other fragments will be at least 15, preferably at least 20, for example at least 25, 30 or 40 nucleotides in length, and are also encompassed by the term polynucleotides of the invention as used herein.

Polynucleotides such as a DNA polynucleotides and probes according to the invention may be produced recombinantly, synthetically, or by any means available to those of skill in the art. They may also be cloned by standard techniques.

In general, primers will be produced by synthetic means, involving a step wise manufacture of the desired nucleic acid sequence one nucleotide at a time. Techniques for accomplishing this using automated techniques are readily available in the art.

Longer polynucleotides will generally be produced using recombinant means, for example using a PCR (polymerase chain reaction) cloning techniques. This will involve making a pair of primers (e.g. of about 15 to 30 nucleotides) flanking a region of the lipid targeting sequence which it is desired to clone, bringing the primers into contact with mRNA or cDNA obtained from an animal or human cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified fragment (e.g. by purifying the reaction mixture on an agarose gel) and recovering the amplified DNA. The primers may be designed to contain suitable restriction enzyme recognition sites so that the amplified DNA can be cloned into a suitable cloning vector.

For expression of the DNA sequence according to the invention it may in some instances be advantageous to incorporate one or more intervening sequences (introns) in the sequence coding for the protein to be expressed, as in some expression systems, one or more splicing events must take place in order to obtain high expression rates (e.g. for expression of a barley thionin in transgenic tobacco; Carmona et al. 1993, Plant J 3, 457-462).

However, in most cases, the coding sequence (i.e. the cDNA), accompanied by the proper regulatory elements, such as promotor and terminator sequences, are sufficient for proper expression.

In a special embodiment (referring to figs 1 and 2), the invention relates to a cDNA sequence, comprising the DNA sequence as given by SEQ ID NO 8 or SEQ ID NO 9, or having a sequence homology with SEQ ID NO 8 or SEQ ID NO 9 of at least 75% or is the complementary sequence thereof. SEQ ID NO 8 is the cDNA sequence of CDC7 of *Arabidopsis thaliana*, comprising the coding sequence for the newly identified amino acid sequences (SEQ ID NOS 2, 3 and 4) as are discussed above. SEQ ID NO 9, is the cDNA sequence of CDC27 of *Arabidopsis thaliana*, includes the sequences coding for the newly identified amino acid sequences (SEQ ID NOS 6 and 7) as discussed above. The presence of the amino acid sequences according to the present invention in DNA replication modulating proteins, in particular in CDC7 and CDC27 respectively, may play an important role in the biological function of the said proteins. Also, the

sequences according to SEQ ID NOS 8 and 9, or parts thereof, can advantageously be used to isolate and identify homologous sequences of other biological species.

In particular, the invention relates to a non-genomic DNA sequence, coding for a peptide according to the invention, corresponding to nucleotides 1229-1291, 2126-2187 or 2298-2385 of SEQ ID NO 8, or to nucleotides 109-181 or 2128-2181 of SEQ ID NO 9, or a DNA sequence, having a sequence homology of at least 75% to the said sequence or the complementary sequence thereof. Such a DNA sequence codes for an amino acid sequence that till now was not known to be part of DNA replication modulating proteins, in particular of CDC7 and CDC27. It was now found, that DNA sequences, corresponding to the nucleotides 1229-1291, 2126-2187 and 2298-2385 of SEQ ID NO 8 code for new amino acid sequences of plant CDC7. The DNA sequence, corresponding to nucleotides 109-181 and 2128-2181 of SEQ ID NO 9 code for novel amino acid sequences of plant CDC27, of *Arabidopsis thaliana*. Said DNA sequences may therefore in particular be used to identify and isolate genes or gene fragments from other plants or organisms that are homologous to the CDC7 or CDC27 sequence discussed above.

Probes and primers

In a further embodiment, the DNA sequences according to the invention may be used as primers for use in a nucleic acid amplification technique. Said primers can be used in a particular amplification technique to identify and isolate substantially homologous nucleic acid molecules from other plant species. The design and use of said primers is known by the person skilled in the art. Preferably such amplification primers comprise a contiguous sequence of at least 6 nucleotides, in particular 13 nucleotides, preferably 15 to 25 nucleotides or more, identical or complementary to the nucleotide sequence encoding the amino acid sequence of SEQ ID Nos 1-7. Another application is the use as a hybridization probe to identify nucleic acid molecules hybridizing with a nucleic acid molecule of the invention by homology screening of genomic DNA or cDNA libraries. Furthermore, the person skilled in the art is well aware that it is also possible to label such a nucleic acid probe with an appropriate marker for

specific applications, such as for the detection of the presence of a nucleic acid molecule of the invention in a sample derived from an organism, in particular plants. A number of companies such as Pharmacia Biotech (Piscataway NJ), Promega (Madison WI), and US Biochemical Corp (Cleveland OH) supply commercial kits and protocols for these procedures. Suitable reporter molecules or labels include those radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles and the like.

The nucleic acid sequence for a protein of the invention can also be used to generate hybridization probes for mapping the naturally occurring genomic sequence. The sequence may be mapped to a particular chromosome or to a specific region of the chromosome using well known techniques. These include in situ hybridization to chromosomal spreads, flow-sorted chromosomal preparations, or artificial chromosome constructions such as yeast artificial chromosomes, bacterial artificial chromosomes, bacterial P1 constructions or single chromosome cDNA libraries as reviewed in Price (Blood Rev. 7 (1993), 127-134) and Trask (Trends Genet. 7 (1991), 149-154).

Vectors

Polynucleotides of the invention can be incorporated into a recombinant replicable vector. The vector may be used to replicate the nucleic acid in a compatible host cell. Thus in a further embodiment, the invention provides a method of making polynucleotides of the invention by introducing a polynucleotide of the invention into a replicable vector, introducing the vector into a compatible host cell, and growing the host cell under conditions which bring about replication of the vector. The vector may be recovered from the host cell. Suitable host cells include bacteria such as *E. coli*, yeast, mammalian cell lines and other eukaryotic cell lines, for example insect Sf9 cells.

Preferably, a polynucleotide of the invention in a vector is operably linked to a control sequence that is capable of providing for the expression of the coding sequence by the host cell, i.e. the vector is an expression vector. The term "operably linked" means that the components described are in

a relationship permitting them to function in their intended manner. A regulatory sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under condition compatible with the control sequences.

The control sequences may be modified, for example by the addition of further transcriptional regulatory elements to make the level of transcription directed by the control sequences more responsive to transcriptional modulators.

Vectors of the invention may be transformed or transfected into a suitable host cell as described below to provide for expression of a protein of the invention. This process may comprise culturing a host cell transformed with an expression vector as described above under conditions to provide for expression by the vector of a coding sequence encoding the protein, and optionally recovering the expressed protein.

The vectors may be for example, plasmid or virus vectors provided with an origin of replication, optionally a promoter for the expression of the said polynucleotide and optionally a regulator of the promoter. The vectors may contain one or more selectable marker genes, for example an ampicillin resistance gene in the case of a bacterial plasmid or a neomycin resistance gene for a mammalian vector. Vectors may be used, for example, to transfect or transform a host cell.

Control sequences operably linked to sequences encoding the protein of the invention include promoters/enhancers and other expression regulation signals. These control sequences may be selected to be compatible with the host cell for which the expression vector is designed to be used in. The term promoter is well-known in the art and encompasses nucleic acid regions ranging in size and complexity from minimal promoters to promoters including upstream elements and enhancers.

The promoter is typically selected from promoters which are functional in mammalian, cells, although prokaryotic promoters and promoters functional in other eukaryotic cells may be used. The promoter is typically derived from promoter sequences of viral or eukaryotic genes. For example, it may be a promoter derived from the genome of a cell in which expression is to occur. With respect to eukaryotic promoters, they may be promoters that function in a ubiquitous manner

(such as promoters of a-actin, b-actin, tubulin) or, alternatively, a tissue-specific manner (such as promoters of the genes for pyruvate kinase). Tissue-specific promoters specific for selected plant tissue cells are particularly preferred, see below in section "transgenic plants".

It may also be advantageous for the promoters to be inducible so that the levels of expression of the heterologous gene can be regulated during the life-time of the cell. Inducible means that the levels of expression obtained using the promoter can be regulated.

In addition, any of these promoters may be modified by the addition of further regulatory sequences, for example enhancer sequences. Chimeric promoters may also be used comprising sequence elements from two or more different promoters described above.

Therefore, the invention relates to DNA vectors, particularly plasmids, cosmids, viruses, bacteriophages and other vectors used conventionally in genetic engineering that comprise a DNA sequence according to the invention. Methods which are well known to those skilled in the art can be used to construct various plasmids and vectors: see for example, the techniques described in Sambrook, Molecular Cloning A Laboratory Manual, Cold Spring Habor Laboratory (1989) N.Y. and Ausubel, Current Protocols in Molecular Biology, Green Publishing Associates and Wiley Interscience, N.Y. (1989), (1994). Said vector further preferably comprises a promoter, functional in plant cells, operably linked to the DNA sequence, according to the invention. With such a vector, the DNA sequence according to the invention can be expressed in plant cells and may modulate the DNA replication in the said cells.

Identifying derivatives, variants and homologs of the c ll cycle interacting proteins of the invention

In another embodiment, the present invention relates to a method for identifying and/or obtaining proteins capable of modulating the DNA repliction in plants, comprising a two-hybrid screening assay, using CDC27 or CDC7 polynucleotide sequences as a bait and a cDNA library of a cell suspension culture as prey.

The yeast two-hybrid assay is a genetic strategy developed to identify proteins (encoded by the cDNAs, the 'preys') able to interact in vivo with a known protein (the 'bait'). Interactions between proteins are detected through the reconstitution of the activity of a transcription activator and the subsequent expression of a reporter gene. The cell culture may be from any organism possessing cell cycle interacting proteins such as animals, preferably mammals. Particularly preferred are plant cell suspension cultures such as from *Arabidopsis*. The nucleic acid molecules encoding proteins or peptides identified to interact with CDC7 or CDC27 in the above mentioned assay can be easily obtained and sequenced by methods known in the art. Therefore, the present invention also relates to a DNA sequence encoding a cell cycle interacting protein obtainable by the method of the invention.

Transgenic plants

To analyse the industrial applicabilities of the invention, transformed plants can be made using the nucleotide sequences according to the invention. Such a transformation of the new gene(s), proteins or inactivated variants/muteins thereof will either positively or negatively have an effect on cell division. Methods to modify the expression levels and/or the activity are known to persons skilled in the art and include for instance overexpression, co-suppression, the use of ribozymes, sense and anti-sense strategies, gene silencing approaches. "Sense strand" refers to the strand of a double-stranded DNA molecule that is homologous to a mRNA transcript thereof. The "anti-sense strand" contains an inverted sequence which is complementary to that of the "sense strand".

Hence, the nucleic acid molecules according to the invention are in particular useful for the genetic manipulation of plant cells in order to modify the characteristics of plants and to obtain plants with modified, preferably with improved or useful phenotypes. Similarly, the invention can also be used to modulate the cell division and the growth of cells, preferentially plant cells, in *in vitro* cultures. A transformed plant can thus be obtained by transforming a plant cell with a gene encoding a polypeptide concerned or fragment thereof alone or in combination. For this purpose tissue specific

promoters, in one construct or being present as a separate construct in addition to the sequence concerned, can be used.

Thus, the present invention relates to a method for the production of transgenic plants, plant cells or plant tissue comprising the introduction of a nucleic acid molecule or vector of the invention into the genome of said plant, plant cell or plant tissue.

The invention further relates to a method for modulating DNA replication in plant cells, plant parts or plants by conferring to one or more plant cells the capacity to provide a protein, or a mutein thereof according to the invention, in an amount sufficient to modulate DNA replication and/or to block mitosis of the said cells.

In particular, the said capacity is conferred to one or more plant cells, by

a) transforming one or more plant cells with DNA according to the invention or with a vector according to the invention,

b) maintain or culture the plant cells in order to regenerate plant parts or plants from the transformed cells

c) incubating the cells, plant parts or plants at conditions, allowing expression of the DNA according to claim 9 or 10, to produce a protein according to the invention or a mutein thereof according to the invention.

For the expression of the nucleic acid molecules according to the invention in sense or antisense orientation in plant cells, the molecules are placed under the control of regulatory elements which ensure the expression in plant cells. These regulatory elements may be heterologous or homologous with respect to the nucleic acid molecule to be expressed as well with respect to the plant species to be transformed. In general, such regulatory elements comprise a promoter active in plant cells. To obtain expression in all tissues of a transgenic plant, preferably constitutive promoters are used, such as the 35 S promoter of CaMV (Odell, Nature 313 (1985), 810-812) or promoters of the polyubiquitin genes of maize (Christensen, Plant Mol. Biol. 18 (1982), 675-689). In order to achieve expression in specific

tissues of a transgenic plant it is possible to use tissue specific promoters (see, e.g., Stockhaus, EMBO J. 8 (1989), 2245-2251). Known are also promoters which are specifically active in tubers of potatoes or in seeds of different plants species, such as maize, Vicia, wheat, barley etc. Inducible promoters may be used in order to be able to exactly control expression. An example for inducible promoters are the promoters of genes encoding heat shock proteins. Also microspore-specific regulatory elements and their uses have been described (WO96/16182). Furthermore, the chemically inducible Tet-system may be employed (Gatz, Mol. Gen. Genet. 227 (1991); 229-237). Further suitable promoters are known to the person skilled in the art and are described, e.g., in Ward (Plant Mol. Biol. 22 (1993), 361-366). The regulatory elements may further comprise transcriptional and/or translational enhancers functional in plants cells. Furthermore, the regulatory elements may include transcription termination signals, such as a poly-A signal, which lead to the addition of a poly A tail to the transcript which may improve its stability.

Methods for the introduction of foreign DNA into plants are also well known in the art. These include, for example, the transformation of plant cells or tissues with T-DNA using *Agrobacterium tumefaciens* or *Agrobacterium rhizogenes*, the fusion of protoplasts, direct gene transfer (see, e.g., EP-A 164 575), injection, electroporation, biolistic methods like particle bombardment, pollen-mediated transformation, plant RNA virus-mediated transformation, liposome-mediated transformation, transformation using wounded or enzyme-degraded immature embryos, or wounded or enzyme-degraded embryogenic callus and other methods known in the art.

In general, the plants which can be modified according to the invention and which either show overexpression of a protein according to the invention or a reduction of the synthesis of such a protein can be derived from any desired plant species. They can be monocotyledonous plants or dicotyledonous plants, preferably they belong to plant species of interest in agriculture, wood culture or horticulture interest, such as crop plants (e.g. maize, rice, barley, wheat, rye, oats etc.),

potatoes, oil producing plants (e.g. oilseed rape, sunflower, pea nut, soy bean, etc.), cotton, sugar beet, sugar cane, leguminous plants (e.g. beans, peas etc.), wood producing plants, preferably trees, etc. The invention further relates to progeny of such plants and to plant material such as roots, flowers, fruit, leaves, pollen, seeds, seedlings or tubers, obtainable from the plant according to the invention.

The invention further relates to a plant cell, transformed with a vector according to the present invention, or comprising DNA according to the present invention. The invention also relates to plants, obtainable by the method according to the present invention and to progeny of such a plant and to plant material, such as roots, flowers, fruit, leaves, pollen, seeds, seedlings or tubers, obtainable from the plant according to the invention.

Mutants

In further embodiments of the invention, expression of dominant negative mutants of CDC7 or CDC27 are used to modulate DNA replication in plant cells, plant tissues, plant organs and/or whole plants. These embodiments involve the overexpression of a mutein or mutant gene according to the present invention which will inhibit the function of a wild-type allele when expressed in the same cell, thereby the phenotype of a transgenic plant, plant organ or plant cell expressing the mutant will be that of a blocked cell cycle progression.

Herskowitz, Nature 329: 219-222 (1987), reviews the inactivation of genes by interference at the protein level, which is achieved through the expression of specific genetic elements encoding a polypeptide comprising both intact, functional domains of the wild type protein as well as nonfunctional domains of the same wild type protein. Such peptides are known as dominant negative mutant proteins. Examples of dominant negative mutants are given below.

CDC7 dominant negative mutant - Nematod resistance

In a special embodiment of the present invention, a DNA vector comprises DNA, coding for a mutein according to the present invention, that is operably linked to a nematode-

induced promoter, said promoter functional in plant cells. Nematode infection of plants may cause severe problems to plant growth and crop generation. After penetrating the roots of their hosts, nematodes induce, at the infection sites, the development of feeding cells, specialised in the uptake of solutes from the vascular system of the plant. These infection sites are of crucial importance for the development for the parasite. In this way, root-knot nematodes induce multinucleated giant cells in the infected plant with highly elevated DNA contents. By specifically blocking the DNA synthesis in the feeding cells, the formation of the said multinucleated giant cells may be blocked, so that the nematodes may not further develop. One can contemplate that a CDC7 mutein, which is not further capable to induce the onset of the DNA synthesis, e.g. by loss of one or more phosphorylation sites or loss of binding function to a plant homolog of yeast DBF4 (Jackson et al 1993 Mol Cell Biol 13, 2899-2908) could, when present in sufficient amounts, block the onset of the DNA synthesis. When DNA, coding for such a mutein, and under the control of a promoter, functional in plant cells and inducible by the presence of nematodes in or in the vicinity of the plant cells, is comprised in the plant cells, the mutein can be expressed in the presence or vicinity of nematodes. This may lead to a DNA synthesis block, therewith avoiding further nematode development. The advantage of such a system is the fact that the plant is not producing any heterologous nematocide, that may be harmful for the plant itself. Such a system is not restricted to CDC7. The person, skilled in the art, aware of this application, will be well aware of the possibilities to take other DNA replication modulating proteins, such as CDC27 for developing an analogous anti-nematode system.

CDC27 mutant - Endoreduplication

A further embodiment of the invention involves the down regulation of CDC27. A further embodiment of the invention involves the downregulation of CDC27 resulting in suppression of the APC complex, modulation of DNA replication and/or blocking mitosis. This can be achieved by expression of CDC27 point mutants. An alternative strategy can be envisaged

involving a CDC27 mutein consisting of a block of TPR tandem repeats. Such a mutein is still likely to interact with other TPR-containing proteins from the APC such as CDC16 and CDC23 or APC regulator proteins such as PP5. As such, APC component proteins or APC regulator proteins would probably be titrated out and normal APC function be prevented. Based on results already obtained from experiments designed to delineate TPR domains involved in the interaction between two TPR proteins (Lamb et al. 1984, EMBO J 13, 4321-4328; Ollendorf and Donoghue 1997, J Biol Chem 272, 32011-32018), this strategy might indeed would prove valuable. Overexpression of CDC27 muteins, via the effect on the APC, can be used to enhance endoreduplication in plant cells, plant tissues, plant organs, or whole plants.

For example, as is described above, a CDC27 mutein wherein the SEQ ID No 7 has been mutated, leading to the incapability of this mutein to bind with other factors of the APC can be mentioned. The mutated protein would be still able to interact with the substrate, therewith titrating out the APC, abolishing or at least seriously reducing the APC-function, leading to the formation of polyploid cells. Also, mutations in SEQ ID No 6 could render the mutein incapable of interacting with the substrate but still capable of binding with the other factors of the APC-complex. The result is the generation of a dominant negative, as the complex will not be able to drive the destruction of key components of the cell cycle machinery, responsible to control the number of DNA-replication cycles.

By manipulating the level of endoreduplication one can increase the storage capacity of, for example, endosperm cells. Thus, another aspect of the current invention is that one or more DNA sequences, vectors or proteins, regulatory sequences or recombinant DNA molecules of the invention can be used to modulate, for instance, endoreduplication in storage cells, storage tissues and/or storage organs of plants or parts thereof.

Preferred target storage organs and parts thereof for the modulation of endoreduplication are, for instance, seeds (such as from cereals,als, oilseed crops), roots (such as in sugar beet), tubers (such as in potato) and fruits (such as in vegetables and fruit species). Furthermore it is expected

that increased endoreduplication in storage organs and parts thereof correlates with enhanced storage capacity and as such with improved yield. In yet another embodiment of the invention, a plant with modulated endoreduplication in the whole plant or parts thereof can be obtained from a single plant cell by transforming the cell, in a manner known to the skilled person, with the above-described means.

CDC27 and CDC7 mutants - Sterile plants

Another embodiment of the invention relates to a method for modulating DNA replication and the resultant generation of male or female sterile plants. This would be achieved by the expression of dominant negative mutants of either cdc7 or cdc27 under the control of very specific promoters - either from male or female gametophytes - to block cell division and disrupt meiosis. The resulting plants would be *naturally* sterile.

Overexpression of CDC7 and DBF4 activate DNA synthesis

Another embodiment of the invention relates to a method for the generation of plant cells, plant tissues, plant organs, or whole plants with the capacity for the overexpression of CDC7 in combination with a plant homolog of Dbf4 thereby modulating DNA replication. Results in yeast indicate that the association of Dbf4 with CDC7 is essential for the G1 to S transition, namely DNA synthesis (Ohtoshi A, Miyake T, Arai K, Masai H; Mol Gen Genet 254(5): 562-70 1997 May 20). Therefore in the present invention, by overexpressing both CDC7 and Dbf4 proteins, one can activate, stimulate or initiate DNA synthesis in cells where DNA synthesis does not normally take place, such as cells that have already gone through the cell cycle. As a consequence the amount of DNA is increased in the cell therewith manipulating the level of endoreduplication as is outlined above.

Polyploid plants

Another embodiment of the invention relates to the generation of polyploid plant cells, plant parts or plants.

If for example, plant cells are transformed with a vector, comprising the coding sequence of plant CDC27, according to the present invention, under the control of a suitable promotor and optionally other expression controlling elements, these plant cells may produce CDC27. When the said plant cells produce CDC27 protein in a sufficient amount, extra rounds of DNA replication may take place before mitosis, leading to polyploid cells.

Characterisation of CDC7 and CD27 genes

The architecture of the CDC7 and CDC27 genes are illustrated in figures 1 and 2. Figure 1 illustrates the genomic architecture of the *Arabidopsis* CDC7 gene, wherein the exons are boxed. The numbers above the box indicate the length of the exon, the number below and between two boxes indicates the length of the intron.

The total length of the coding sequence is 2667 nucleotides, coding for 889 amino acids. The fifth, eleventh and thirteenth exons comprise novel coding sequence; in figure 1, the corresponding boxes are black. It is to be understood, and obvious to a skilled person, that the first and the last triplet of the coding sequence of an exon, may partially be encoded by the last two or one nucleotide(s) from the adjacent downstream exon, and, accordingly, by the first two or one nucleotide(s) of the adjacent upstream exon. In figure 2, the genomic architecture of the CDC27 gene of *Arabidopsis thaliana* is depicted as explained for figure 1. The second and the sixteenth (last) exon (black in figure 2) comprise novel coding sequences and were not identified in the known genomic CDC27 sequence of *Arabidopsis thaliana* (see text). The entire sequence comprises 2187 nucleotides, corresponding to 728 amino acids.

In figures 3 and 4, the complete cDNA sequence of CDC7 and CDC27, respectively, according to the present invention are depicted, with the respective encoded amino acid sequence therebelow. Vertical lines in the nucleotide sequence indicate the exon boundaries, i.e. $^{2}|^{3}$ is the boundary between exons 2 and 3. The exon boundaries are derived from genomic CDC7 and CDC27 sequences (see examples

1 and 2 respectively). Such lines are also drawn in the amino acid sequence, although, as is indicated above, the amino acids, flanking such a vertical line, may be partially encoded by the adjacent exon. Exact positioning of the vertical line is in such a case not possible and is set at the left or the right of such an amino acid in an arbitrary manner. See examples 1 and 2 for further details.

The invention will now be further illustrated by the following examples, that are not intended to limit the scope of the invention.

EXAMPLES

Although in general the techniques mentioned herein are well known in the art, reference may be made in particular to Sambrook *et al.*, Molecular Cloning, A Laboratory Manual (1989) and Ausubel *et al.*, Current Protocols in Molecular Biology (1995), John Wiley & Sons, Inc. Further, scientific explanations and reasonings in the examples are given for illustrative reasons only, without however being bound thereto.

Example 1.

ISOLATION OF AN ARABIDOPSIS CDC7 HOMOLOGUE

Conserved regions of the *Saccharomyces cerevisae* and *Schizosaccharomyces pombe* CDC7 homologue genes were used to synthesize degenerated oligonucleotides to amplify an *Arabidopsis* CDC7 homologue cDNA fragment. These oligonucleotides were as follows:

1 (sense):
5'AAA/G ATA/C/T GGA/C/G/T GAA/G GGA/C/G/T ACA/C/G/T TT 3'

2 (sense):
5' ATA/C/T ATA/C/T CAC/T AGA/G GAA/G ATA/C/T AA 3'

3 (antisense)
5' AG C/TTC A/C/G/TGG A/C/G/TGC C/TCT A/GAA A/C/G/TCC 3'

4 (antisense)
5' AC A/C/G/TCC A/C/G/TA/GC A/GCT CCA A/C/G/TAT A/GTC 3'

First strand cDNA prepared from whole *Arabidopsis* plants using the Superscript Preamplification System from Life Technologies was used as template in nested PCR reactions. The first reaction was carried using the pair of oligos 1 and 4, and the second reaction used oligos 2 and 3. PCR conditions were essentially as described (Ferreira et al. 1991). A fragment of approximately 650 bp was eluted from an agarose gel, cloned in pGEM-T and sequenced. Sequencing comparison using the GCG-package version 9.1

showed that the deduced amino acid sequence of the PCR fragment has approximately 40% homology to the published yeast CDC7 sequences. This fragment was then used to screen a lambda gt10 cDNA library prepared from total *Arabidopsis* plants. The largest cDNA isolated, approximately 1,2 kb, was completely sequenced by the dideoxy method. This *Arabidopsis* cDNA contains an open reading frame encoded encoding a polypeptide of 384 amino acids (amino acid 473 to amino acid 856 in figure 3). With the SRS search program the EMBL and EMBLnew databanks were screened for gene sequences designated or annotated with the term cdc7. One genomic sequence from *Arabidopsis thaliana* was found (accession number Z97342). This submitted genomic sequence comprised a predicted gene, indicated as "having similarity to protein kinase HSK of fission yeast", having 11 exons and coding for a protein having 829 amino acids.

With the GCG-package version 9.1, the said genomic sequence was compared with the identified partial cDNA sequence, using the "best-fit program". The identified cDNA-sequence covered nucleotides 119827 to 121978 of the genomic sequence of Z97342.

The identified cDNA-sequence did not correspond with the complete coding sequence of the predicted gene on the Z97342 sequence. Within the present cDNA sequence, two additional coding sequences (additional exons) were identified, namely nucleotides no 120770-120709 and 120350-120263 of Z97342, coding for the amino acid sequences of SEQ ID NOS 3 and 4 respectively.

Upon comparison with the genomic *Arabidopsis sequence*, it however appeared that the present cDNA was not complete. To complete our cDNA at the 5' side we used the CAP-finder kit (Clontech), using the primers (CTCTCCCATCTGGTCATGTC, #1; GAACATGCAGTAGCCGTACC, #2) specified for the cDNA, in nested PCR reactions. For the missing 3' end, two nested sequences specific for the cDNA (AAATGGTGCGAACTCAACAC, #2) and (TATGGGAAGTAGCCAAGCTG, #1) and an anchored oligo-dT on the lower strand were used. PCR conditions were essentially as described (Ferreira et al., 1991). The fragments were eluted from agarose gel and cloned using standard techniques and sequenced. The deduced amino acid sequence encoded by

the PCR fragment showed clear homology to the yeast published CDC7 sequences and matched with an the above mentioned *Arabidopsis* genomic sequence. The DNA-fragment, comprising the missing 5' terminal sequence, comprised an additional coding sequence of 63nt (nrs 122340 to 122278 in Z97342) not identified in Z97342, coding for the amino acid sequence of SEQ ID NO 2.

With the obtained sequences, the complete cDNA for the CDC7 homologue of *Arabidopsis thaliana* could be reconstructed, which is illustrated in figure 3 and in SEQ ID NO 8.

The presently identified CDC7 cDNA comprises additional novel coding sequences, corresponding to novel exons (nos 5, 11 and 13 in figure 3), that were not identified in Z97342, and codes for a protein of 890 amino acids.

Example 2. ISOLATION OF AN ARABIDOPSIS CDC27 HOMOLOGUE

Conserved regions of the published CDC27 homologue genes (Sikorski et al., 1991 Cold Spring Harbor Symposia on Quantitative Biology vol LVI, 663-673, 1991) were used to synthesize degenerated oligonucleotides to amplify *Arabidopsis* CDC27 cDNA. The oligonucleotides were as follows:

1 (sense):

5' TGG GTA/C/G/T TTA/G GCA/C/G/T A/CAA/G GG 3'

2 (sense):

5' ATG GAA/C/G/T G/ATT/C/A TA/TC/T AGA/C/G/T AC 3'

3 (antisense)

5' AGA/G CAT/C TAT/C AAT/C GCA/C/G/T TGG 3'

4 (antisense)

5' TA T/A/G AC/T CAT A/C/G/TCC C/TAA A/C/G/CC A/GAA 3'

First strand cDNA prepared from flower buds was used as template in nested PCR reactions. The first reaction was carried using the pair of oligos 1 and 4, and the second reaction used oligos 2 and 3. PCR conditions were as described (Ferreira et al., 1991, Plant Cell 3, 531-540), except that the annealing temperature of the first reaction was 45 C, and for the second reaction, 37 C was used. A

fragment of approximately 300 bp was eluted from agarose gel and cloned in pGEM-T. Out of 16 clones sequenced, two showed high homology to published CDC27 sequences (Sikorski et al., 1991 Cold Spring Harbor Symposia on Quantitative Biology vol LVI, 663-673, 1991). This fragment was then used to screen a lambda gt10 cDNA library prepared from total *Arabidopsis* plants. The isolated target cDNA, approximately 2,5 kb, was completely sequenced by the dideoxy method and is shown in fig 4 and in SEQ ID nr 9. A combination of restriction enzymes and oligonucleotide subcloning was used to produce the templates for sequencing.

The *Arabidopsis* CDC27 cDNA contains one open reading frame, encoding a polypeptide of 728 amino acids (figure 4). With the SRS search program, the databanks EMBL and EMBL new were screened for gene sequences, homologous to the present CDC27 cDNA sequence. A genomic sequence from *Arabidopsis thaliana* (accession number AC001645) was found, comprising 14 exons, coding for a protein of 728 AA. With the GCG-package version 9.1, the present cDNA-sequence was compared with the said genomic *Arabidopsis* sequence (1) using the "best fit"-program. It appeared that the present cDNA comprised additional coding information for two novel exons, namely the second and last exon of the *Arabidopsis* CDC27-gene (exons 2 and 16 in fig 4).

The amino acid sequences encoded by the second and last exon are depicted in SEQ ID NOS 6 and 7 respectively.

Example 3 DOMINANT NEGATIVE MUTANTS OF CDC7

Dominant negative mutants of CDC7 (CDC7 DN) are constructed by creating substitution mutations including amino acid residues 1(G), 5(V), 18(A) and 20(K) of SEQ ID No2; amino acid residues 13(T), 16(F), 18(A) and 20(E) of SEQ ID No3; amino acid residues 7(L) and 18(K) of SEQ ID No4. Substitutions are not conservative. Expression of a CDC7 DN in a whole plant, a plant tissue, a plant organ or a plant cell results in cell cycle arrest at G1/S. These results are in line with the situation in yeast, wherein one such substitution, threonine 13 of SEQ ID No 3 (position 722 in SEQ ID No 1) to a glutamate has proven to create a dominant

negative CDC7 in yeast. This CDC7 DN is inactive as a kinase but can still bind DBF4, thus preventing activation of wild-type CDC7 molecules (Ohtoshi et al. 1997, Mol Gen Genet 254, 562-570).

The CDC7 DN mutants can be obtained by site-directed mutagenesis using the ExSite PCR-based site-directed mutagenesis kit (Stratagene, La Jolla, CA). Fidelity of the mutagenesis are confirmed by sequencing.

Example 4 MUTANTS OF CDC27

Several types of CDC27 muteins can be considered:

(1) Insertion of an amino acid such as proline (P) in the amino acid sequence SEQ ID No 7, e.g. behind the tyrosine (Y) residue leads to a loss-of-function of the APC. It is believed that such an insertion deforms the predicted (α-helix of the novel TPR-like domain of which SEQ ID No 7 is part and causes a disturbance of the overall three-dimensional structure of CDC27, therewith titrating out functional proteins of the APC, such as CDC16 or CDC 23, leading to loss of APC function. In line with these results, altering the α-helix structure in one of the TPR units of yeast CDC27 has been proven, and of any of the TPR units has been hypothesized, to destroy CDC27 function (Lamb et al. 1984, EMBO J. 13, 4321-4328).

(2) Deletion of the NH2-terminal 200 to 220 amino acids of CDC27 also leads to loss of function of the APC by titrating out molecules such as APC substrates or APC regulators. This domain encompasses the conserved amino acid sequence SEQ ID No 6 as well as the first TPR unit of CDC27. Deletion of this sequence in human CDC27 abrogates binding of e.g. CDC16, but not of that of e.g. PP5, an APC regulator protein (Ollendorf and Donoghue 1997, J Biol Chem 272, 32011-32018).

(3) CDC27 muteins consisting of the conserved NH2-terminal domain (containing SEQ ID No6) and 1, 2 or more of the downstream TPR units.

(4) CDC27 muteins consisting of the novel TPR-like domain (ending with SEQ ID No7) preceded by 1, 2 or more of

the upstream TPR units.

Muteins described in (3) and (4) act as those described in (1) or (2).

The point mutants in (1) are obtained by site-directed mutagenesis using the ExSite PCR-based site-directed mutagenesis kit (Stratagene, La Jolla, CA). Fidelity of the mutagenesis are confirmed by sequencing. Deletion mutants in (2), (3) and (4) are obtained by high-fidelity PCR (Expand High Fidelity PCR System, Boehringer, Mannheim) using primers designed to amplify the desired stretches of the CDC27 nucleotide sequence. Primers include extensions recognized by restriction endonucleases to allow easy cloning in a vector such as pUC18. Amplified sequences are checked by nucleotide sequence determination.

Expressing such CDC27 muteins in a whole plant, a plant tissue, a plant organ or a plant cell will cause malfunctioning of the APC and thus repetitive cycles of DNA synthesis without intervening mitosis. This endoreduplication results in a polyploid phenotype.

Example 5 NEMATODE RESISTANCE - CDC7 DN

In order to obtain nematode resistance, the CDC7 DN coding sequence is operably linked to a plant promoter responsive to nematode infection and to the NOS polyadenylation site. The ARM1 or Att0728 promoters can be used (Barthels et al. 1997, Plant Cell 9, 2119-2134). The CDC7 DN expression cassette is subsequently transferred to a binary vector such as pGSC1704 and the resulting vector electroporated into *Agrobacterium tumefaciens* C58C1RifR (pGV2260). Transformants are selected on streptomycin/spectinomycin containing medium and checked for the presence of the integral transformed binary vector. *Arabidopsis thaliana* Col-0 is transformed with the selected *A. tumefaciens* strain by the floral dip method (Clough and Bent 1998, Plant J 16, 735-743). Transgenic plants are selected after seed germination in the presence of hygromycin. Selected transgenic lines and untransformed control lines are infected with root knot or cyst nematodes. Successfulness of infection is scored

linking CDC7 DN or CDC27 mutein to a tapetum specific promoter such as Osg6B (Tsuchiya et al. 1995, Plant Cell Physiol 36, 487-494) and to a NOS polyadenylation site will result in a suitable expression cassette. Introduction of this cassette into *A. thaliana* is done as described in example 5. Selected transformant lines have a reduced and/or abnormal pollen formation/development. This is assessed using microscopic methods.

Example 7 - ENDOREDUPLICATION - CDC27 muteins

Any of the muteins are operably linked to a constitutive promoter such as the CaMV 35S promoter (Kay et al. 1987, Science 236, 1299-1302) or to a seed endosperm-specific promoter such as from a 2S albumin seed storage protein (Guerche et al. 1990, Plant Cell 2, 469-478) or to the BLZ2 promoter (Carbonero et al, 1999 in press) and to a polyadenylation signal. Such expression cassettes are transferred to *A. thaliana* as described in example 5. Selected transformant lines have a general higher rate of endoreduplicating cells (CaMV 35S promoter) and/or produce seeds with a higher amount of polyploid endosperm cells (2S albumin promoter). Endoreduplication or polyploidism is assessed in several ways.

(1) Confocal microscopy is applied to measure the nuclear diameter. Polyploid cells normally have enlarged

nuclei in order to harbor the increased DNA content.

(2) The DNA content of plant cells is measured by flow cytometry (Galbraith et al. 1991, Plant Physiol 96, 985-989).

(3) The cyclin B-degrading activity of the APC is determined as described by King et al. (1995, Cell 91, 279-288).

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:
(A) NAME: CropDesign NV
(B) STREET: Technologiepark 3
(C) CITY: Zwijnaarde-Gent
(D) STATE: none
(E) COUNTRY: Belgium
(F) POSTAL CODE (ZIP): 9052

(ii) TITLE OF INVENTION: Plant DNA replication modulating proteins

(iii) NUMBER OF SEQUENCES: 9

(iv) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy Disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: Wordperfect 5.2

(2) INFORMATION FOR SEQ ID NO: 1;

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 889 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY : linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: No

(ix) FEATURE:
(A) NAME/KEY: CDC7
(B) LOCATION:
(xi) SEQUENCE DESCRIPTION:

1 MSENSEPRQL ENSTAGRELI PLSPTNSDGN DDLNYHLHAF ELSRLLLSSG

51 HPESVIDLSS KCTYFQGSPN LVKYLCSIPN SPISLAEDGF TVTLSPESPS

101 APASFACSLD LQENVVLEQF MDPRSLTLKH SRENAEQEEL ELMPLPKRSR

151 NDGNDVNYSV IDSRPNDIRT VACGTMLGTI LALESQASVF NLSASNRGIE

201 AFVQDHQPGP QTSNASVDVN PTHRLEESKN DLPSPQEDGY YERPEIGDFQ

251 IADNQILIEE GDDKNKKDLF PKGEIQTDSV QSDPVASLMP TENELEPVQI

301 VDDTEDLLVD DHTVDIVSTP DRELPLKPSA TEANQDKSLV QKTLDQCKLP

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351  GNSKTYSCSP EIKHTRKSKV IQKRKQNFNT VRLKDQKDQA KHNTIPDFDS

401  YTIVEEEGSG GYGIVYKATR KTDGTEFAIK CPHVGAQKYY VNNEIRMLER

451  FGGKNCIIKH EGCLKNGDSD CIILEHLEHD RPDSLKREID VYQLQWYGYC

501  MFKALSSLHK QGVVHRDVKP GNFLFSRKTN KGYLIDFNLA MDLHQKYRRA

551  DKSKAASGLP TASKKHHTLV KSLDAVNRGT NKPSQKTLAP NSIKKAAGKT

601  RARNDMTRWE RLNSQGAEGS GLTSAKDVTS TRNNPSGEKR REPLPCHGRK

651  ALLDFLQETM SVPIPNHEVS SKAPTSMRKR VAALPGKAEK ELLYLTPMPL

701  CSNGRPEAGD VIEKKDGPCS GTKGFRAPEV CFRSLHQGPK IDVWSAGVTL

751  LYLIMGRTPF TGDPEQNIKD IAQLRGSEEL WEVAKLHNRE SSFPKELYES

801  RYLKGMELRK WCELNTKRRE FLDVIPLSLL DLVDKCLTVN PRRRISAEDA

851  LKHDFFHPVH ETLRNQMLLK QQPTVVADAV SQTLNYLQL
```

(2) INFORMATION FOR SEQ ID NO: 2;

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION:

GYGIVYKATRKTDGTEFAIK

(2) INFORMATION FOR SEQ ID NO: 3;

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION:

DVIEKKDGPCSGTKGFRAPE

(2) INFORMATION FOR SEQ ID NO: 4;

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION:

NIKDIAQLRGSEELWEVAKLHNRESSFPK

(2) INFORMATION FOR SEQ ID NO: 5;

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 728 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: CDC27
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION:

Seq id no 5

1 MMENLLANCV QKNLNHFMFT NAIFLCELLL AQFPSEVNLQ LLARCYLSNS

51 QAYSAYYILK GSKTPQSRYL FAFSCFKLDL LGEAEAALLP CEDYAEEVPG

101 GAAGHYLLGL IYRYSGRKNC SIQQFRMALS FDPLCWEAYG ELCSLGAAEE

151 ASTVFGNVAS QRLQKTCVEQ RISFSEGATI DQITDSDKAL KDTGLSQTEH

201 IPGENQQDLK IMQQPGDIPP NTDRQLSTNG WDLNTPSPVL LQVMDALPPL

251 LLKNMRRPAV EGSLMSVHGV RVRRRNFFSE ELSAEAQEES GRRRSARIAA

301 RKKNPMSQSF GKDSHWLHLS PSESNYAPSL SSMIGKCRIQ SSKEVIPDTV

351 TLNDPATTSG QSVSDIGSSV DDEEKSNPSE SSPDRFSLIS GISEVLSLLK

401 ILGDGHRHLH MYKCQEALLA YQKLSQKQYN THWVLMQVGK AYFELQDYFN

451 ADSSFTLAHQ KYPYALEGMD TYSTVLYHLK EEMRLGYLAQ ELISVDRLSP

501 ESWCAVGNCY SLRKDHDTAL KMFQRAIQLN ERFTYAHTLC GHEFAALEEF

551 EDAERCYRKA LGIDTRHYNA WYGLGMTYLR QEKFEFAQHQ FQLALQINPR

601 SSVIMCYYGI ALHESKRNDE ALMMMEKAVL TDAKNPLPKY YKAHILTSLG

651 DYHKAQKVLE ELKECAPQES SVHASLGKIY NQLKQYDKAV LHFGIALDLS

701 PSPSDAVKIK AYMERLILPD ELVTEENL

(2) INFORMATION FOR SEQ ID NO: 6;

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION:

VNLQLLARCYLSNSQAYSAYYILK

(2) INFORMATION FOR SEQ ID NO: 7;

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION ID 7:

AYMERLILPDELVTEENL

(2) INFORMATION FOR SEQ ID NO: 8;

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2670 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(ix) FEATURE:
(A) NAME/KEY: CDC7
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION:

```
   1  ATGTCAGAAA ACTCGGAACC GCGTCAACTC GAGAATTCTA CAGCCGGAAG

  51  AGAGCTCATT CCTCTTAGTC CCACCAATTC AGACGGCAAC GACGACCTTA

 101  ACTATCATCT GCATGCTTTT GAGTTATCTC GTCTCCTACT TTCTTCTGGT

 151  CATCCAGAAT CTGTTATAGA TCTTTCTTCA AAGTGTACAT ACTTCCAAGG

 201  TTCTCCTAAT CTCGTCAAAT ATCTTTGCTC GATCCCTAAT TCTCCTATTT

 251  CCCTTGCCGA AGATGGCTTC ACTGTGACTC TCTCGCCTGA GTCTCCCTCC

 301  GCTCCGGCTA GTTTCGCCTG TAGTTTGGAT TTGCAGGAAA ATGTTGTGTT

 351  AGAACAGTTT ATGGATCCGA GATCTCTCAC GCTAAAGCAT TCGAGAGAGA

 401  ATGCGGAACA AGAGGAGCTA GAGCTCATGC CATTGCCCAA AAGAAGTCGA

 451  AATGATGGAA ACGATGTGAA TTACTCTGTA ATAGATAGCA GACCTAACGA

 501  CATCAGAACT GTTGCCTGTG GAACTATGCT TGGGACTATT TTAGCTCTTG

 551  AATCCCAAGC TTCGGTTTTC AATTTAAGTG CATCTAACCG AGGAATAGAG

 601  GCTTTTGTTC AAGATCATCA GCCTGGTCCG CAGACATCCA ATGCTTCAGT

 651  GGATGTCAAT CCTACACATC GGTTAGAGGA AAGCAAGAAC GATTTGCCAT

 701  CTCCTCAGGA GGATGGATAT TACGAGCGAC CTGAAATTGG AGATTTCCAA
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751 ATTGCTGACA ACCAAATATT AATCGAAGAA GGTGATGATA AAAATAAGAA

801 GGATCTCTTC CCTAAGGGAG AGATACAAAC TGATTCTGTG CAGTCCGATC

851 CCGTTGCCTC ATTGATGCCA ACAGAAAATG AGTTAGAACC AGTGCAGATT

901 GTGGATGACA CTGAAGATCT ACTTGTAGAT GATCACACTG TAGACATCGT

951 TAGCACCCCT GACAGAGAGC TGCCGTTGAA GCCTTCTGCT ACAGAAGCTA

1001 ATCAAGATAA ATCTTTGGTA CAAAAAACTC TGGATCAATG CAAATTGCCG

1051 GGAAACAGCA AAACGTACAG CTGTTCCCCT GAGATAAAAC ACACCAGAAA

1101 AAGTAAAGTT ATCCAGAAGA GGAAGCAGAA TTTTAACACC GTTCGTCTTA

1151 AAGATCAGAA GGATCAGGCA AAGCATAACA CAATTCCAGA TTTTGATTCT

1201 TACACTATTG TAGAGGAAGA AGGTTCAGGT GGCTACGGGA TTGTTTATAA

1251 GGCAACGAGG AAAACTGATG GAACAGAGTT TGCAATTAAA TGCCCTCATG

1301 TTGGCGCTCA GAAGTATTAT GTGAATAATG AAATCAGAAT GCTGGAGCGT

1351 TTTGGGGGGA AAAACTGTAT AATAAAGCAT GAAGGCTGTC TCAAGAATGG

1401 AGATTCTGAT TGCATCATCC TTGAGCACCT TGAACATGAC AGACCTGATT

1451 CATTGAAGAG AGAAATAGAT GTGTATCAGC TGCAGTGGTA CGGCTACTGC

1501 ATGTTCAAAG CTCTATCGAG TCTGCATAAG CAGGGTGTTG TTCATAGGGA

1551 TGTTAAGCCA GGAAACTTCC TCTTCTCTAG GAAGACCAAC AAAGGCTATC

1601 TCATTGATTT TAACCTTGCC ATGGATTTGC ACCAGAAGTA CAGAAGAGCA

1651 GATAAATCAA AAGCAGCTTC AGGTCTTCCT ACCGCCAGCA AGAAACATCA

1701 TACATTGGTT AAATCACTCG ATGCGGTAAA CCGAGGGACC AACAAACCTT

1751 CTCAGAAAAC TTTAGCGCCT AATAGTATCA AGAAAGCAGC GGGAAAGACA

1801 AGAGCTCGGA ATGACATGAC CAGATGGGAG AGACTCAATA GCCAAGGGGC

1851 AGAAGGGTCT GGCTTAACTT CAGCTAAAGA TGTGACCAGC ACAAGGAACA

1901 ACCCTTCAGG TGAAAAGAGA AGAGAGCCTT TGCCATGTCA TGGAAGAAAA

1951 GCGCTTTTAG ATTTTCTGCA AGAGACAATG TCTGTTCCAA TTCCAAACCA

2001 TGAAGTATCA TCCAAAGCTC CTACGTCTAT GAGAAAACGG GTAGCTGCTC

2051 TTCCAGGGAA AGCTGAGAAG GAACTTCTTT ATCTGACCCC AATGCCACTG

2101 TGCTCTAACG GTCGGCCTGA AGCAGGGGAC GTAATTGAGA AGAAAGACGG

2151 TCCTTGCTCA GGAACCAAAG GCTTCCGAGC TCCAGAGGTT TGCTTCAGAT

2201 CTTTGCACCA AGGACCTAAG ATAGACGTGT GGTCTGCGGG AGTTACTTTG

2251 TTATACCTCA TAATGGGAAG GACACCTTTC ACTGGTGACC CTGAACAGAA

2301 CATAAAGGAC ATTGCACAAC TACGAGGCAG TGAAGAATTA TGGGAAGTAG

2351 CCAAGCTGCA CAACCGTGAA TCCTCTTTCC CTAAGGAATT ATACGAGTCA

2401 AGGTACTTGA AGGGGATGGA GTTGAGAAAA TGGTGCGAAC TCAACACAAA

2451 ACGCAGAGAG TTTCTAGACG TAATTCCACT ATCGCTTCTT GACCTCGTTG

2501 ATAAATGTTT GACCGTTAAC CCGAGGCGAC GAATCAGCGC AGAGGATGCT

2551 CTCAAGCACG ACTTCTTCCA TCCAGTACAT GAAACCCTTA GAAACCAAAT

2601 GCTCCTTAAA CAGCAGCCTA CAGTGGTTGC TGACGCAGTA AGCCAAACTC

2651 TAAACTATTT ACAATTGTAA

(2) INFORMATION FOR SEQ ID NO: 9;

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2187 nucleotides
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: No

(ix) FEATURE:
(A) NAME/KEY: CDC27
(B) LOCATION:

(xi) SEQUENCE DESCRIPTION:

```
1     ATGATGGAGA ATCTACTGGC GAATTGTGTC CAGAAAAACC TTAACCATTT

51    TATGTTCACC AATGCTATCT TCCTTTGCGA ACTTCTTCTC GCCCAATTTC

101   CATCTGAGGT GAACCTGCAA TTGTTAGCCA GGTGTTACTT GAGTAACAGT

151   CAAGCTTATA GTGCATATTA TATCCTTAAA GGTTCAAAAA CGCCTCAGTC

201   TCGGTATTTA TTTGCATTCT CATGCTTTAA GTTGGATCTT CTTGGAGAGG

251   CTGAAGCTGC ATTGTTGCCC TGTGAAGATT ATGCTGAAGA AGTTCCTGGT

301   GGTGCAGCTG GGCATTATCT TCTTGGTCTT ATATATAGAT ATTCTGGGAG

351   GAAGAACTGT TCAATACAAC AGTTTAGGAT GGCATTGTCA TTTGATCCAT

401   TGTGTTGGGA AGCATATGGA GAACTTTGTA GTTTAGGTGC CGCTGAAGAA

451   GCCTCAACAG TTTTCGGGAA TGTTGCTTCC CAGCGTCTTC AGAAAACTTG

501   TGTAGAACAA AGAATAAGCT TCTCAGAAGG AGCAACCATA GACCAGATTA

551   CAGATTCTGA TAAGGCCTTA AAAGATACAG GTTTATCGCA AACAGAACAC

601   ATTCCAGGAG AGAACCAACA AGATCTGAAA ATTATGCAGC AGCCTGGAGA
```

651 TATTCCACCA AATACTGACA GGCAACTTAG TACAAACGGA TGGGACTTGA

701 ACACACCTTC TCCAGTGCTT TTACAGGTAA TGGATGCTCT ACCGCCTCTG

751 CTTCTTAAGA ATATGCGTCG TCCAGCAGTG GAAGGATCTT TGATGTCTGT

801 ACATGGAGTG CGTGTGCGTC GAAGAAACTT TTTTAGTGAA GAATTGTCAG

851 CAGAGGCTCA AGAAGAATCT GGGCGCCGCC GTAGTGCTAG AATAGCAGCA

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951 ACATCTTTCA CCTTCCGAGT CAAACTATGC ACCTTCTCTT TCCTCGATGA

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CLAIMS

1. At least partially purified protein, capable of modulating DNA replication in plants, at least comprising in the amino acid sequence

a) one or more of the amino acid sequences chosen from the group consisting of those, given by SEQ ID NOS 2, 3 and 4,

b) one or more of the amino acid sequences chosen from the group consisting of those, given by SEQ ID NOS 6 and 7,

c) one or more amino acid sequences having at least 50% amino acid identity with those of a), or

d) one or more amino acid sequences having at least 50% amino acid identity with those of b).

2. Protein according to claim 1, comprising one or more of the amino acid sequences according to c) or d), the respective amino acid identity being at least 90%.

3. Protein according to claim 1 or 2, having the amino acid sequence as given in SEQ ID 1 or no 5, or having at least 80% amino acid identity with one of the said sequences.

4. Protein according to one or more of claims 1-3, being a plant CDC7 protein or a functional analogue thereof.

5. Protein according to one or more claims 1-3, being a plant CDC27 protein or a functional analogue thereof.

6. Mutein of a protein according to one or more of the preceding claims, comprising at least one amino acid substitution, deletion or addition, affecting the DNA replicative effect of the said protein.

7. Mutein according to claim 6, wherein at least one of the phosphorylatable amino acids are deleted or substituted by one or more non-phosphorylatable amino acids.

8. Peptide, comprising

a) one or more of the amino acid sequences chosen from the group consisting of those given by SEQ ID No 2, 3 and 4,

b) one or more of the amino acid sequences chosen from the group consisting of those, given by SEQ ID NOS 6 and 7,

c) one or more amino acid sequences having at least 50% amino acid identity with those of a), or

d) one or more amino acid sequences having at least 50% amino acid identity with those of b).

9. Antibody, specifically recognizing a protein according to any of the claims 1-5, a mutein according to any of the claims 6-7 or a peptide according to claim 8.

10. Antibody according to claim 9, being at least partially purified.

11. Non-genomic DNA sequence coding for a protein according to one or more of claims 1-5, for a mutein according

to claim 6 or 7, or for a peptide according to claim 8, or DNA sequence having a sequence homology of at least 75% of the said sequence or the complementary DNA sequence thereof.

12. DNA sequence according to claim 11, being substantially free of sequences intervening the coding sequence.

13. DNA sequence according to claim 11 or 12, comprising the DNA sequence as given by SEQ ID no 8 or SEQ ID no 9 or having a sequence homology with SEQ ID no 8 or SEQ ID no 9 of at least 75% or the complementary sequence thereof.

14. DNA sequence, coding for a peptide according to claim 8, corresponding to nucleotides 1229-1291, 2126-2187 or 2298-2385 of SEQ ID No 8, or to nucleotides 109-181 or 2128-2181 of SEQ ID No 9, or a DNA sequence, having a sequence homology of at least 75% to the said sequence or the complementary sequence thereof.

15. DNA vector, at least comprising the DNA sequence according to one of the claims 11-14.

16. DNA vector according to claim 15, further comprising a promoter, functional in plant cells, operably linked to the DNA sequence according to one of the claims 11-14.

17. DNA vector according to claim 15 or 16 comprising DNA coding for a mutein according to claim 6 or 7, operably linked to a nematode-induced promoter, functional in plant cells.

18. Method for modulating DNA replication in plant cells, plant parts or plants by conferring to one or more plant cells the capacity to provide a protein according to one or more of claims 1-5, or a mutein thereof according to claim 6 or 7, in an amount sufficient to modulate DNA replication and/or to block mitosis of the said cells.

19. Method according to claim 18, wherein the said capacity is conferred to one or more plant cells, by

a) transforming one or more plant cells with DNA according to one of the claims 9-12 or with a DNA vector according to one of the claims 13-15,

b) culturing the plant cells in order to regenerate plant parts or plants from the transformed cells, or

c) incubating the cells, plant parts or plants at conditions allowing expression of the said DNA to produce the said protein or a mutein.

20. Method according to claim 18 or 19 for the generation of polyploid plant cells, plant parts or plants.

21. Method for identifying and/or obtaining proteins capable of modulating the DNA replication in plants, comprising a two-hybrid screening assay, using CDC27 or CDC7 polynucleotide sequences as a bait and a cDNA library or of a cell suspension culture as a prey.

22. Method for the production of transgenic plants, plant cells or plant tissue, comprising the introduction of a nucleic acid molecule according to any of the claims 11-14 or a vector

according to claim 15 or 16 into the genome of said plant, plant cell or plant tissue.

23. Plant cell, transformed with a vector according to one of the claims 15-16, or comprising the DNA according to one of the claims 11-14.

24. Plant, obtainable by the method according to one or more of claims 18-19.

25. Progeny of a plant according to claim 24.

26. Plant material such as roots, flowers, fruit, leaves, pollen, seeds, seedlings or tubers, obtainable from a plant according to claim 24 or 25.

A B S T R A C T

The present invention relates to at least partially purified protein, capable of modulating the DNA replication in plants, muteins thereof, DNA coding therefor and to a method to confer to one or more plant cells the capacity to provide such a protein or mutein. The invention also relates to plants, comprising the said DNA and the progeny thereof.

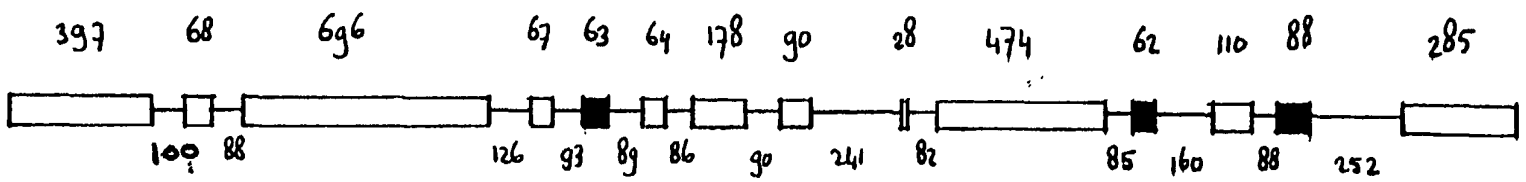


Fig. 1

CDC 7

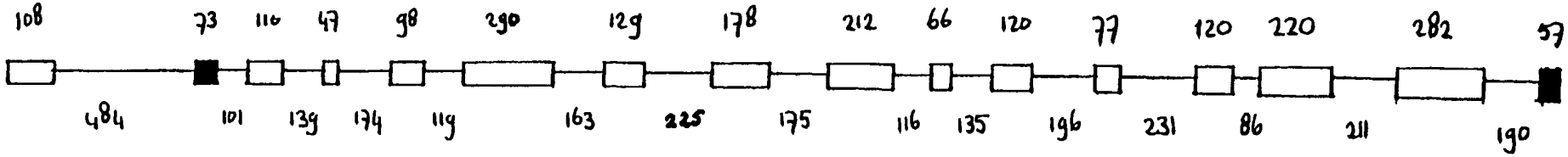
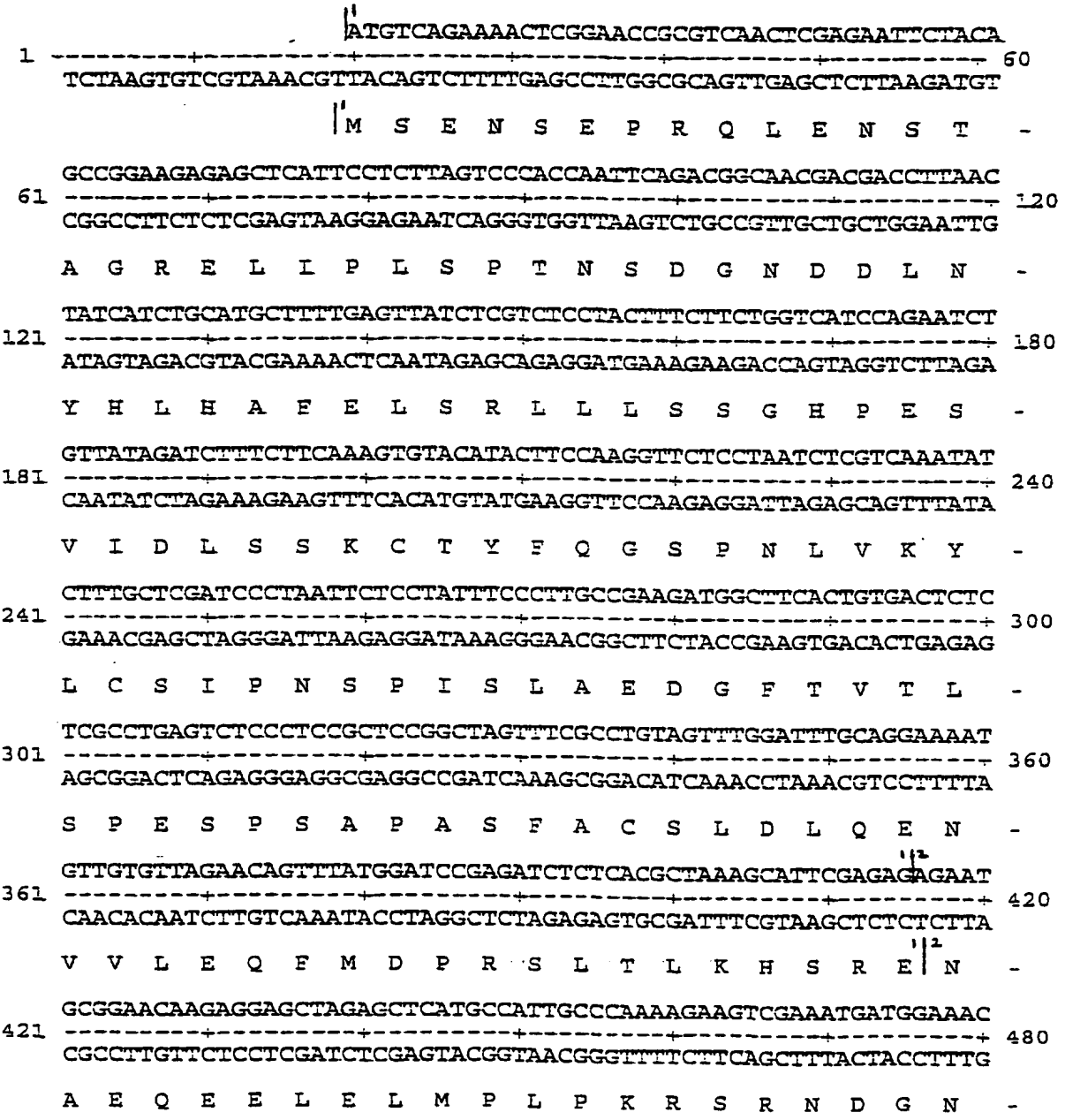


Fig. 2

CDC 27

Fig. 3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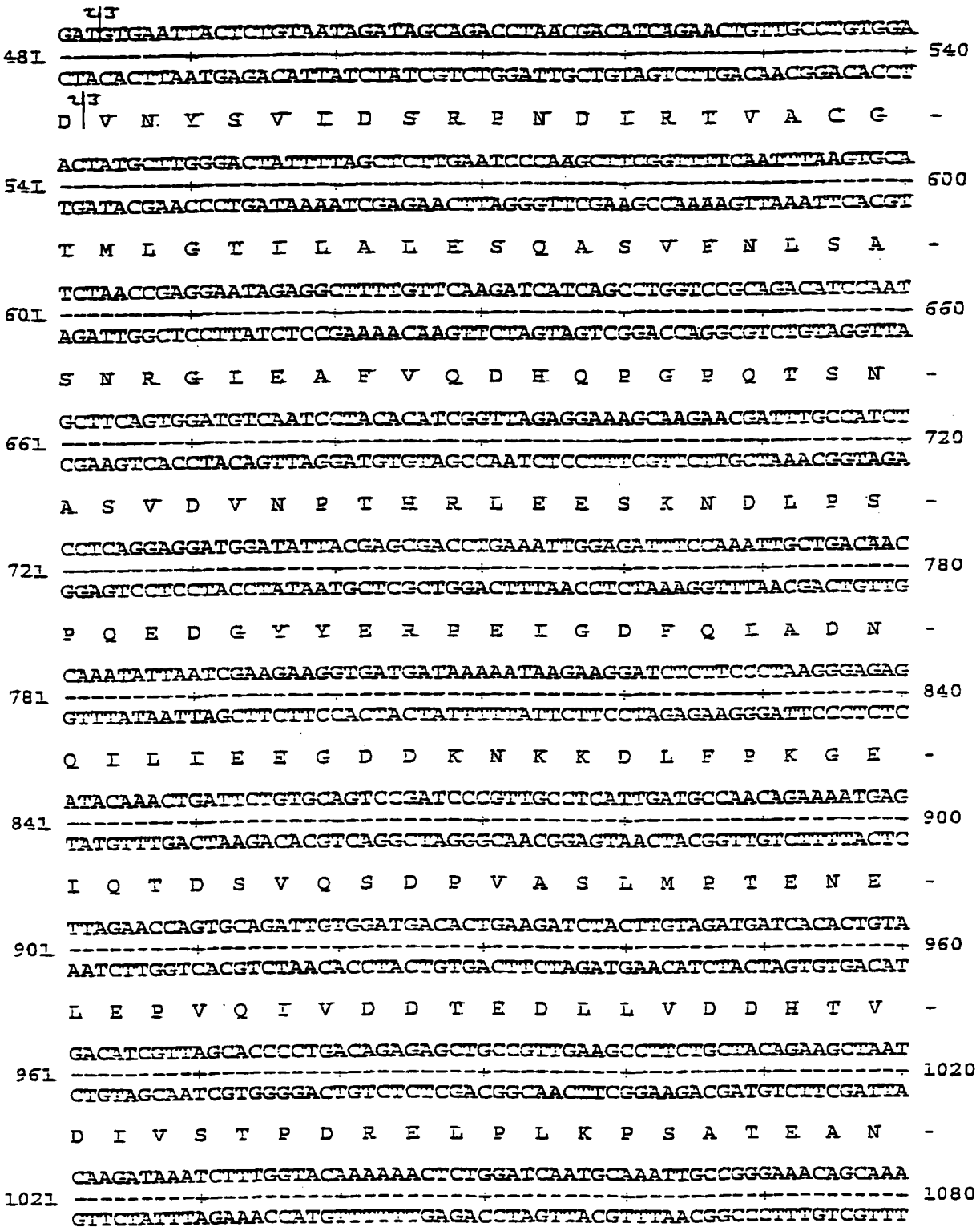
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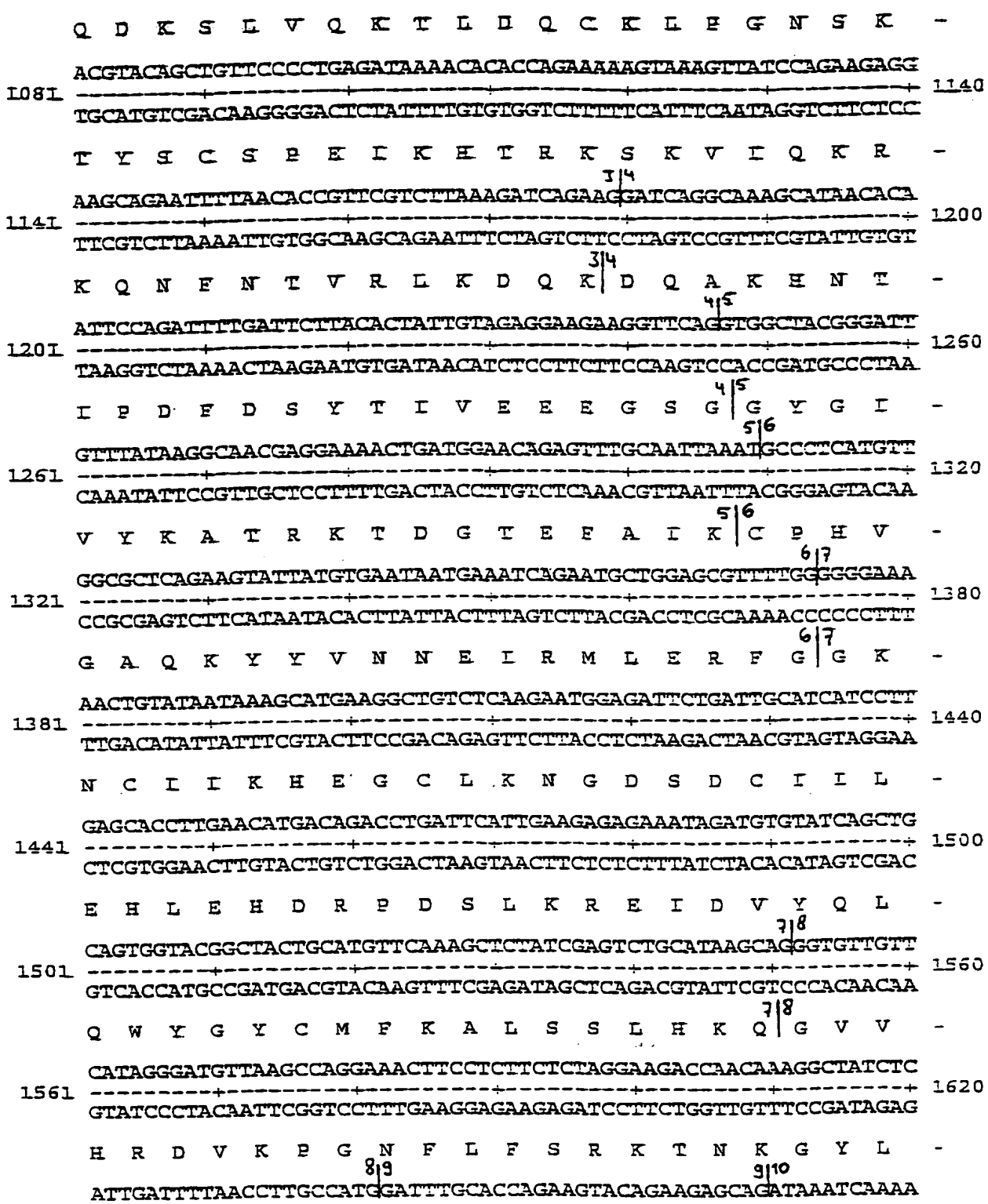
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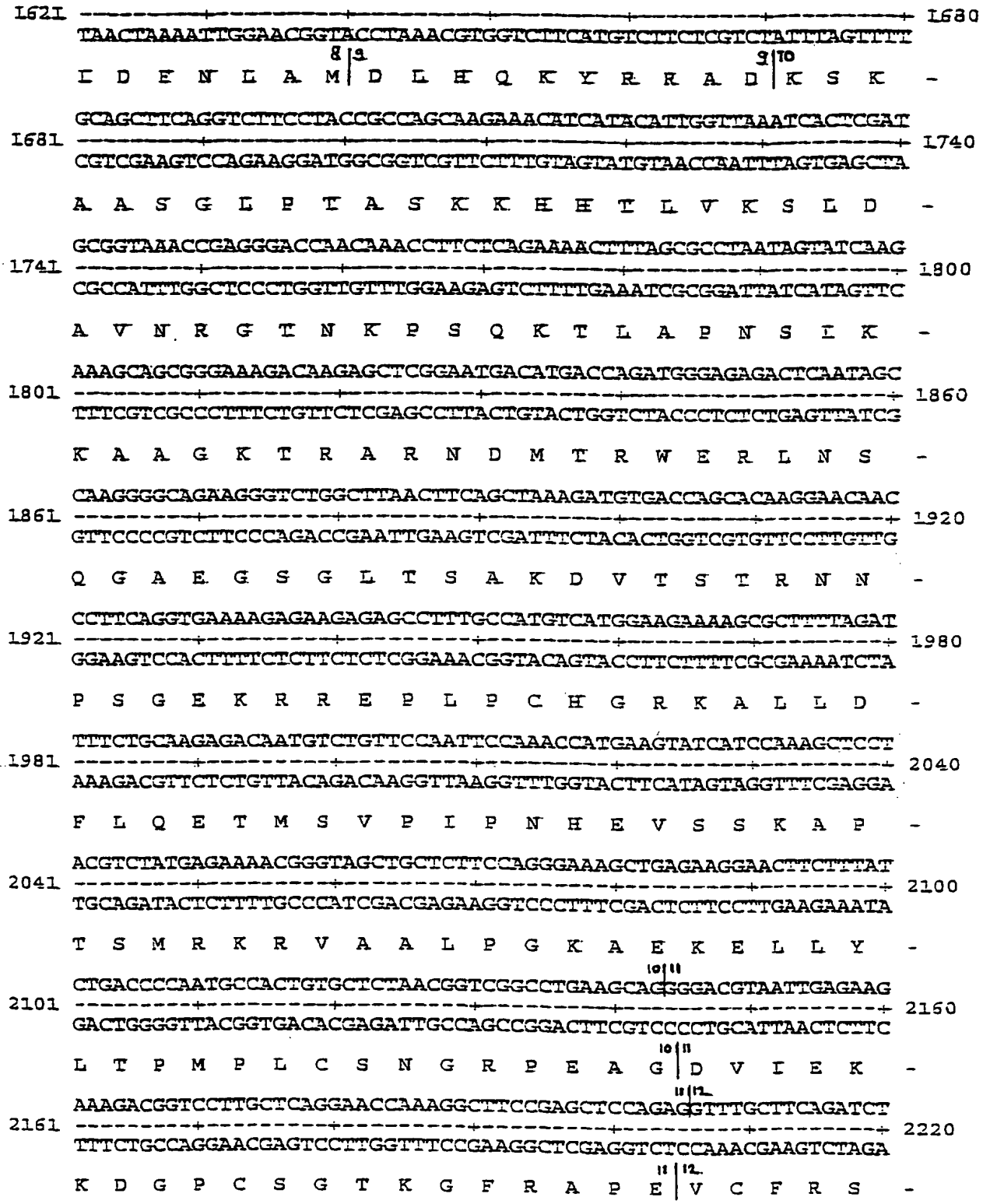
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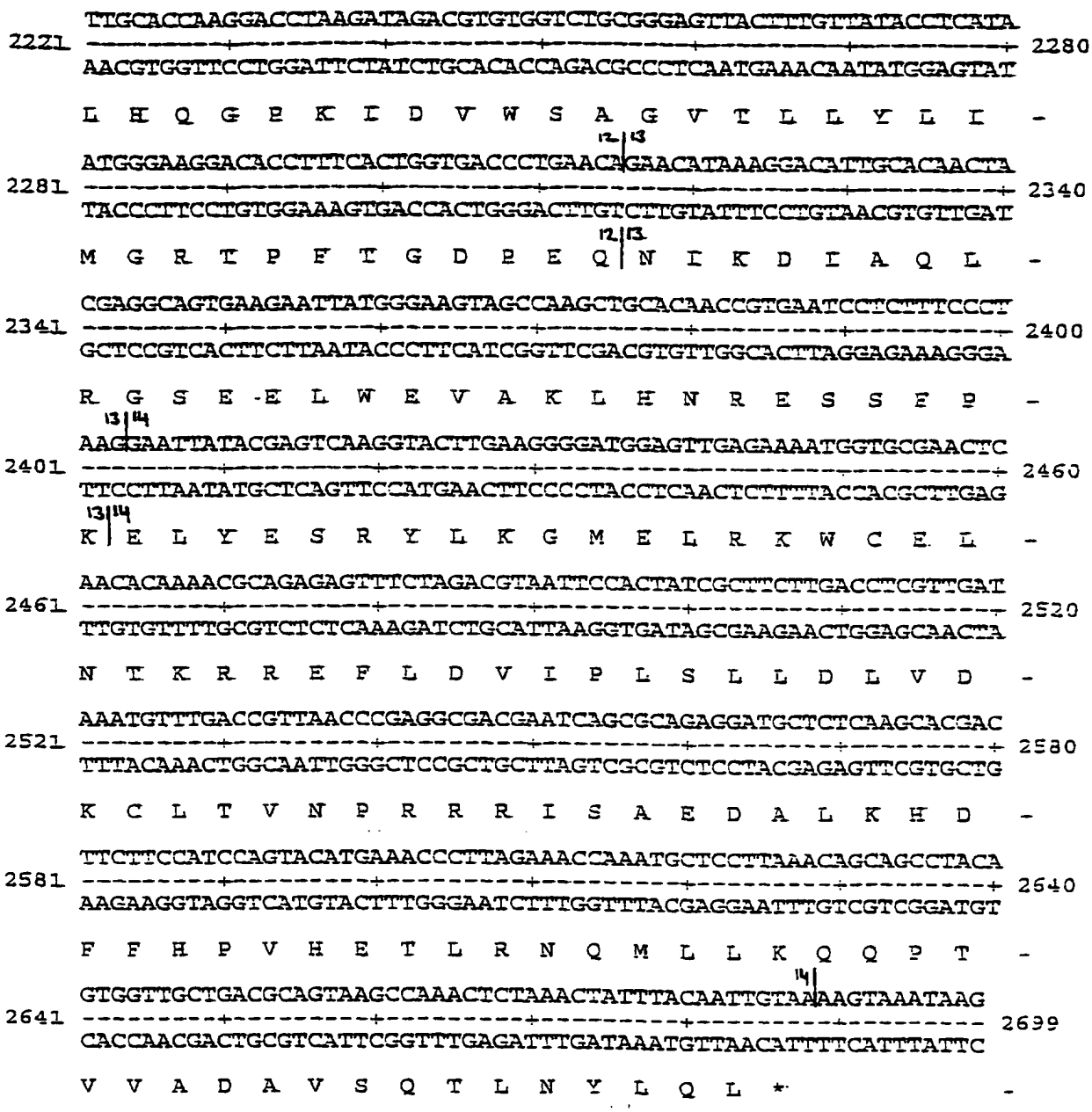
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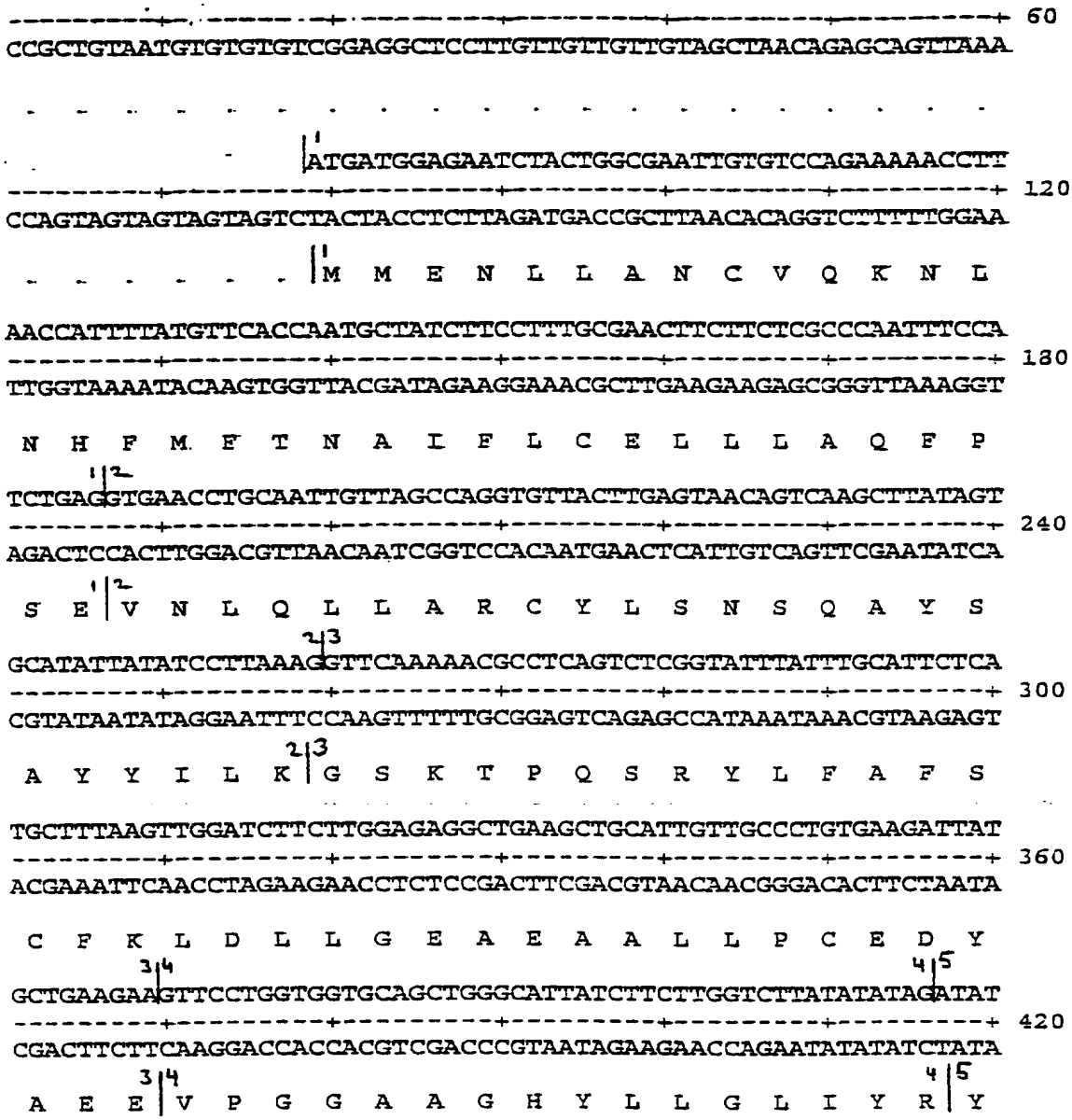
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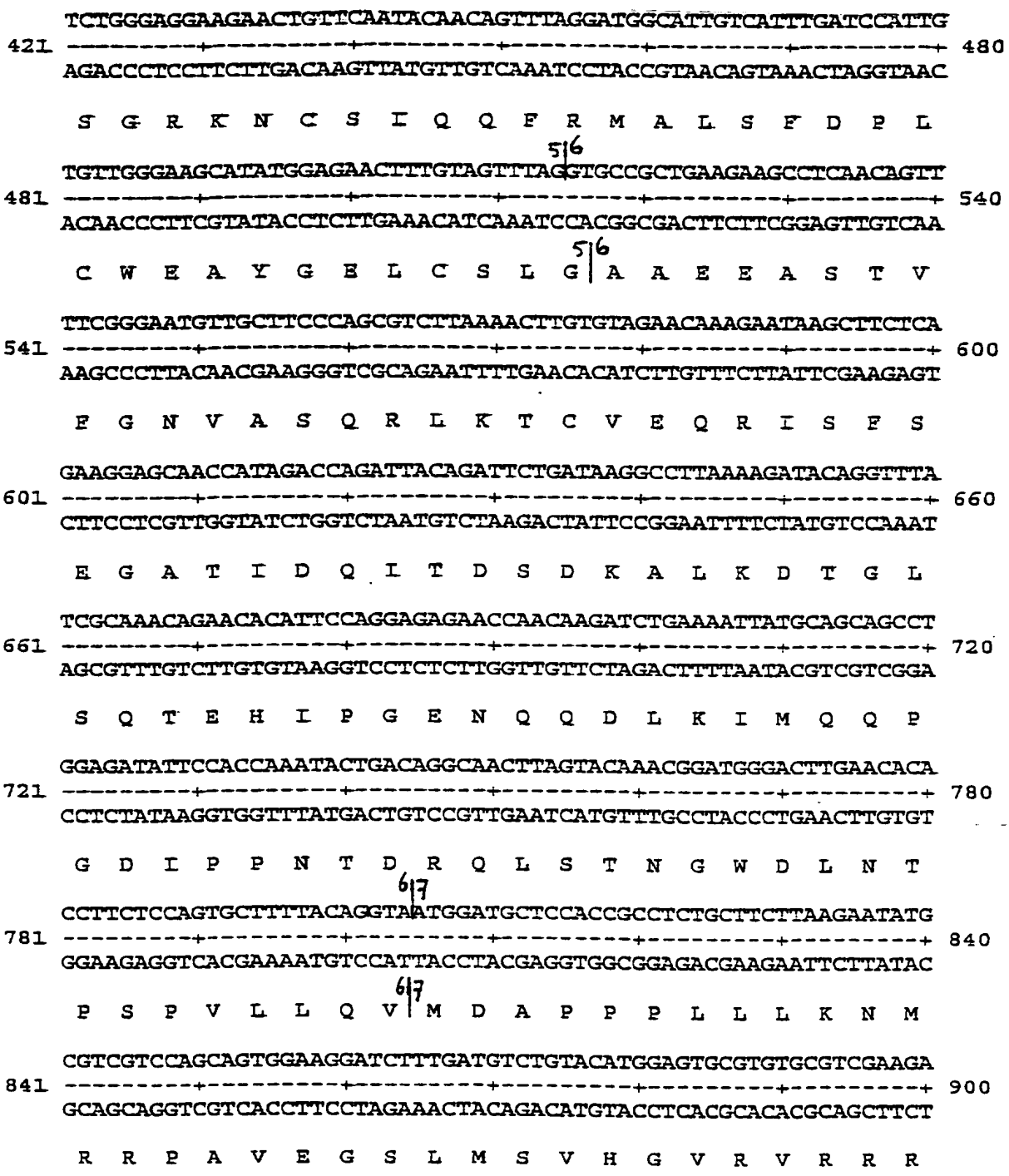
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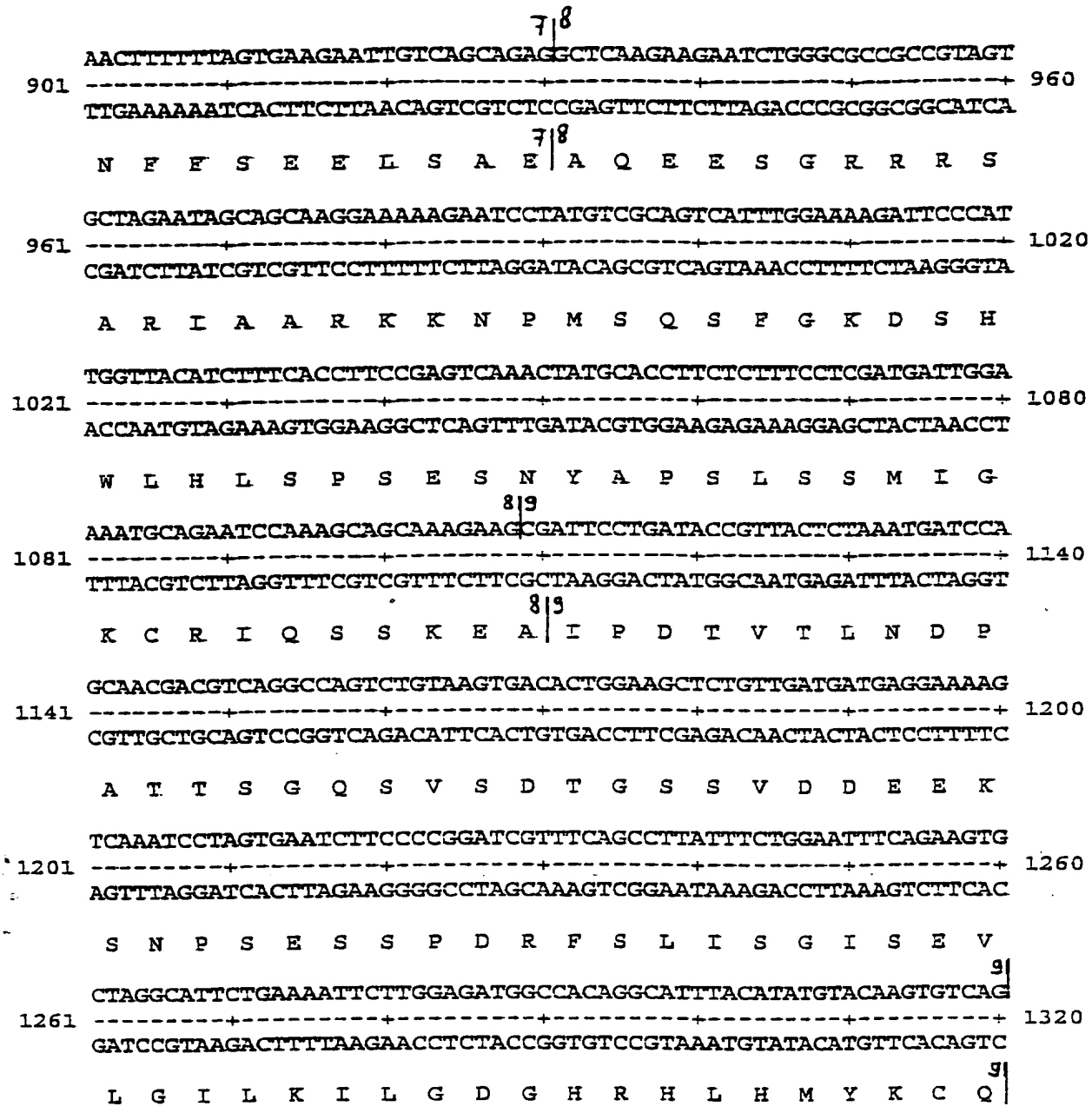
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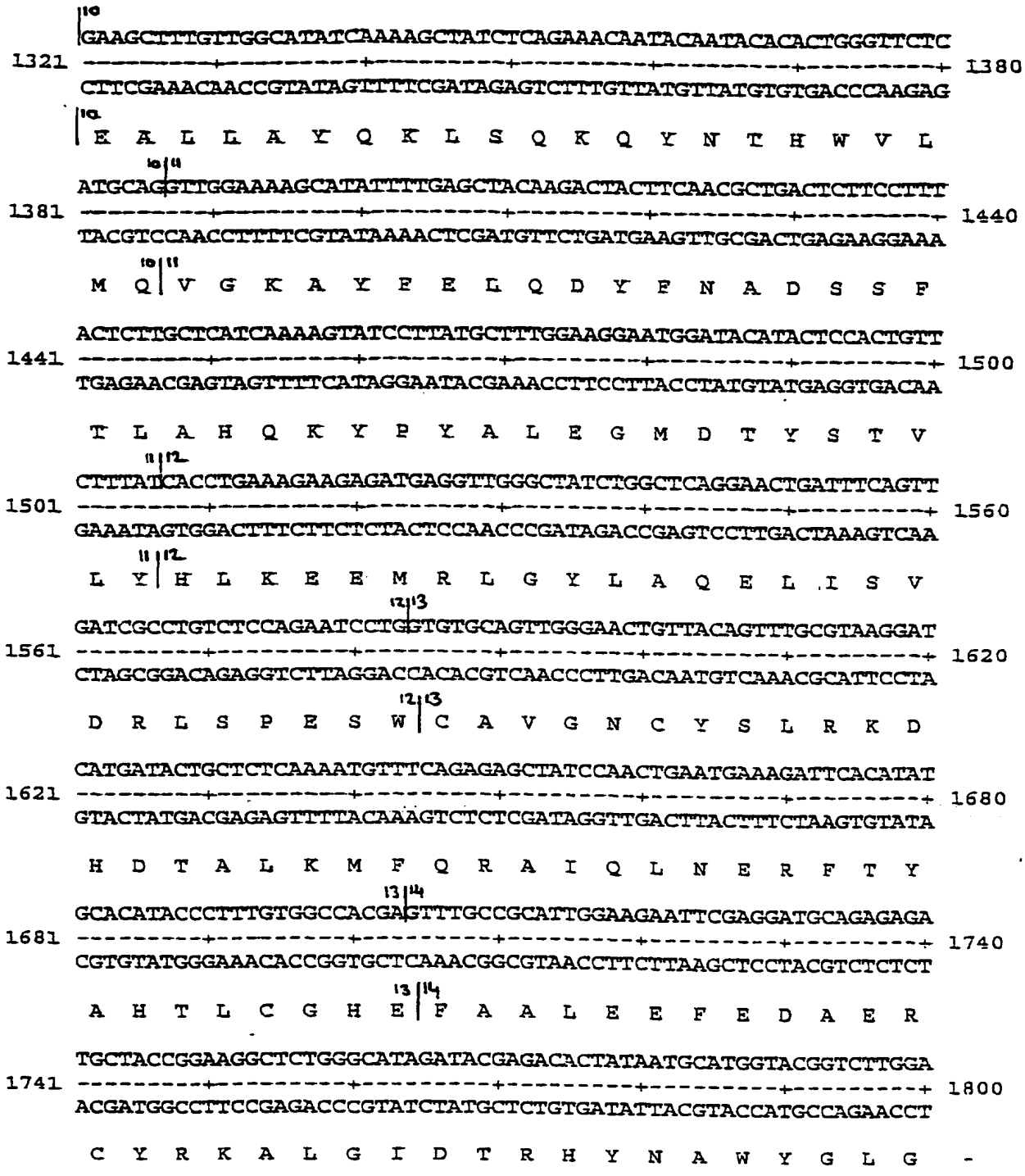
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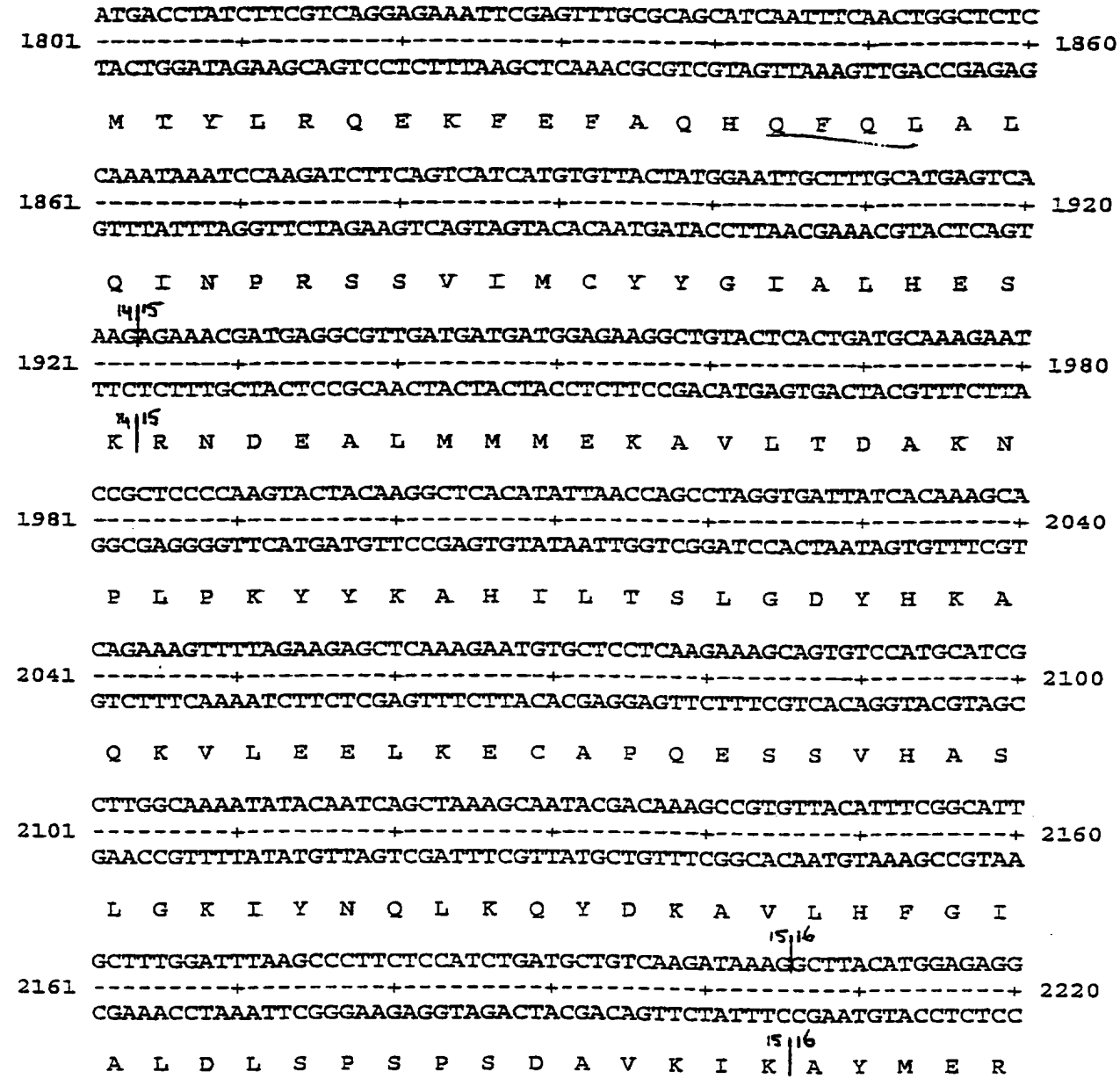
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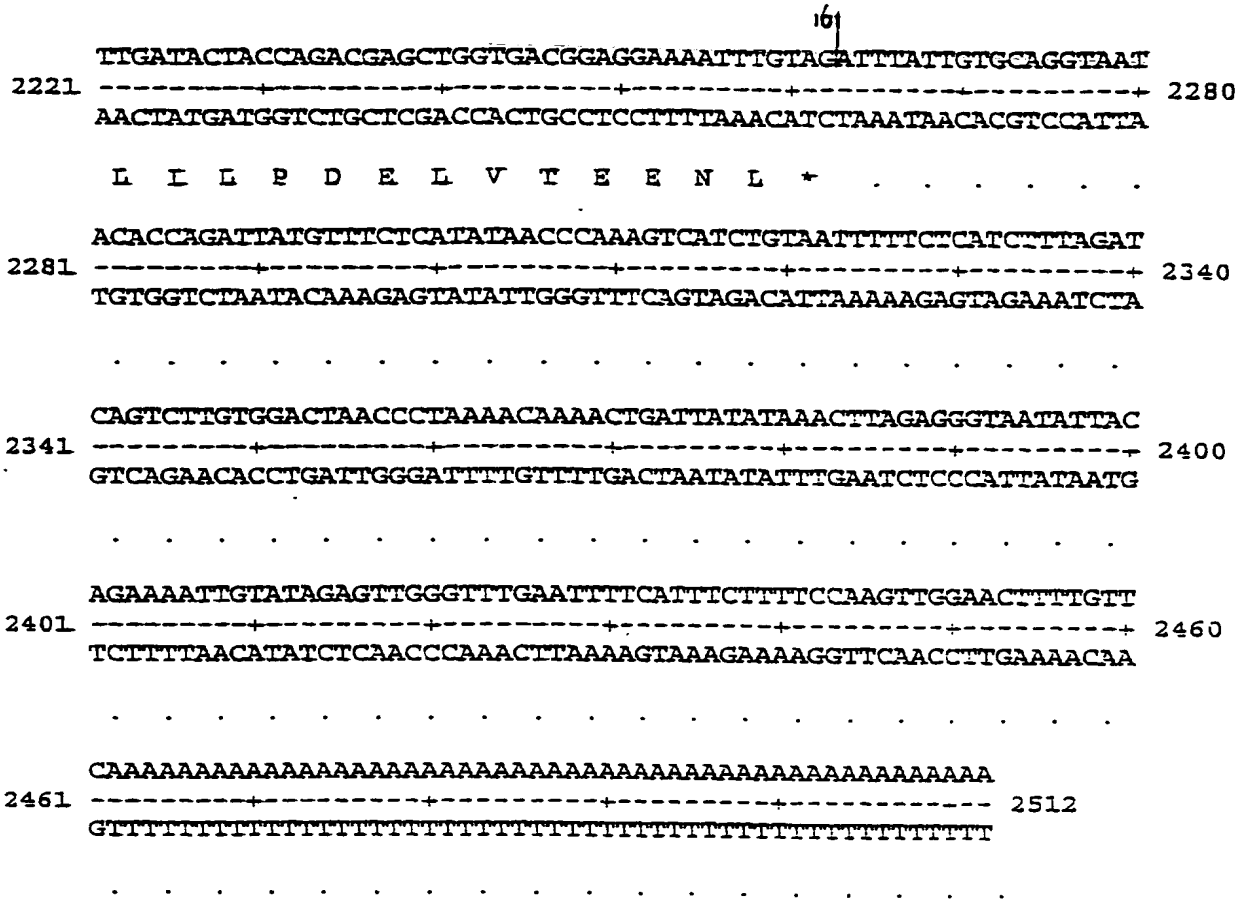
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